

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:38 ; Search time 130 Seconds
(without alignments)
94.635 Million cell updates/sec

Title: US-10-088-417A-1
Perfect score: 132
Sequence: 1 KIAALKQKIASLKQIDALEYENDALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 9880

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	28	AAB74343	Aab74343 Peptide S
2	132	100.0	28	AAB74351	Aab74351 Peptide S
3	132	100.0	28	ADM41436	Adm41436 Self-asse
4	129	97.7	28	AAB74341	Aab74341 Peptide S
5	129	97.7	28	AAB74342	Aab74342 Peptide S
6	85	64.4	28	ADM41438	Adm41438 Self-asse
7	82	62.1	28	AAB74345	Aab74345 Peptide S
8	76	57.6	28	AAB74348	Aab74348 Peptide S
9	76	57.6	28	AAB74356	Aab74356 Peptide S
10	76	57.6	28	AAB74352	Aab74352 Peptide S
11	75	56.8	28	AAB74346	Aab74346 Peptide S
12	75	56.8	28	AAB74347	Aab74347 Peptide S
13	74	56.1	28	AAB74349	Aab74349 Peptide S
14	70	53.0	28	AAB74350	Aab74350 Peptide S
15	70	53.0	28	AAB74355	Aab74355 Peptide S
16	57	43.2	28	ABR84737	ABR84737 DE novo d
17	54	40.9	28	ABR84736	ABR84736 DE novo d
18	51	38.6	28	AAB50879	Aab50879 Integrin
19	51	38.6	28	AAB59138	Aab59138 Alpha-bel
20	46	34.8	28	AAR31979	Aar31979 SSP4 poly
21	45	34.1	28	ABR84735	ABR84735 DE novo d
22	41	31.1	28	ADT02245	Adt02245 Surface p
23	40	30.3	28	AAR31981	Aar31981 SSP7 poly
24	40	30.3	28	AAR78256	Aar78256 SSP(7)4 h

25	40	30.3	28	6	ADA15966	Ada15966 Synthetic
26	40	30.3	28	6	ABO44343	AbO44343 Ear I-bas
27	40	30.3	28	9	ADM71693	Adm71693 Peptide S
28	38	28.8	28	2	AAR76756	Aar76756 E. coli F
29	37	28.0	28	2	AAR32693	Aar32693 SSP poly
30	37	28.0	28	2	AAR32689	Aar32689 SSP poly
31	37	28.0	28	2	AAR31980	Aar31980 SSP5 poly
32	37	28.0	28	2	AAR78255	Aar78255 SSP(5)4 h
33	37	28.0	28	2	AAR78250	Aar78250 SSP 5.5.5
34	37	28.0	28	2	AAR78244	Aar78244 SSP 5.5.5
35	37	28.0	28	2	AAR78242	Aar78242 SSP 5.5.5
36	37	28.0	28	2	AAR62935	Aar62935 Minimalis
37	37	28.0	28	2	AAW62947	Aaw62947 Minimalis
38	37	28.0	28	2	AAW60508	Aaw60508 Synthetic
39	37	28.0	28	2	AAW60516	Aaw60516 Synthetic
40	37	28.0	28	2	AAW60510	Aaw60510 Synthetic
41	37	28.0	28	2	AAW87744	Aaw87744 Synthetic
42	37	28.0	28	2	AAW87746	Aaw87746 Synthetic
43	37	28.0	28	2	AAW87748	Aaw87748 Synthetic
44	37	28.0	28	4	AAE11041	Aae11041 Leucine z
45	37	28.0	28	4	AAE11042	Aae11042 Leucine z

ALIGNMENTS

RESULT 1
AAB74343
ID AAB74343 standard; peptide; 28 AA.
XX AC AAB74343;
XX AC
XX AC
DT 02-JUL-2001 (first entry)
XX XX
DE Peptide SAF-plC.
XX XX
KW Atomic Force Microscopy; AFM.
XX OS
XX Unidentified.
XX WO200121646-A1.
XX PD
XX 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX XX
XX (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX Claim 16; Page 26; 45pp; English.
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-plC
XX Sequence 28 AA;
SQ

Query Match 100.0%; Score 132; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIAALKQKIASLKQIDALEYENDALEQ 28

PT tissue engineering, or constructing nanoscale molecular sieves.
XX Claim 16; Page 26; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1A
XX
SQ Sequence 28 AA;

Query Match 97.7%; Score 129; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 8e-11; Indels 0; Gaps 0;
Matches 27; Conservative 1; Mismatches 0;
Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
Db 1 KIAALKQKIASLKQIEDALEYENDALEQ 28

RESULT 5
AAB74342
ID AAB74342 standard; peptide; 28 AA.
XX
AC AAB74342;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p1B.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
PN WO200121646-A1.
XX
PD 29-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-GB003576.
XX
PR 17-SEP-1999; 99GB-00022013.
XX
PA (UYSU-) UNIV SUSSEX.
XX
PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX
DR New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Page 9; 45pp; English.
XX
CC The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p1B
XX
SQ Sequence 28 AA;

Query Match 97.7%; Score 129; DB 4; Length 28;
Best Local Similarity 96.4%; Pred. No. 8e-11;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
Db 1 KIAALKQKIASLKQIEDALEYENDALEQ 28

RESULT 6
AAB74345
ID AAB74345 standard; peptide; 28 AA.
XX
AC AAB74345;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2A.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.

ADM41438
ID ADM41438 standard; peptide; 28 AA.
XX
AC ADM41438;
XX
DT 03-JUN-2004 (first entry)
XX
DE Self-assembling peptide fibre SAF-p2a.
XX
KW Fibre-shaping peptide; self-assembling peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal NH3 moiety"
FT
XX WO2004022584-A1.
XX
PN 18-MAR-2004.
XX
PD 08-SEP-2003; 2003WO-GB003900.
XX
PF 06-SEP-2002; 2002GB-00020805.
XX
PR (UYSU-) UNIV SUSSEX.
XX
PA Woolfson D, Ryadnov MG;
XX WPI; 2004-248444/23.
XX
DR Novel fiber-shaping peptide comprising hub and several peptide monomer
XX units, useful for producing protein structure useful in purification of
XX biological fluids and in surface engineering procedures.
XX
SQ Example 36; Page 22; 37pp; English.
XX
CC The present sequence is that of self-assembling peptide fibre (SAF) SAF-
XX p2a. The invention relates to fibre-shaping (Fish) peptides ADM41434-
XX ADM41435 that are capable of interacting with SAFs to form protein
XX structures. The Fish peptides allow morphological changes (branches,
XX splits, kinks and bends) to be made to protein fibres comprising SAFs. By
XX incorporating such morphological changes in the protein structures, it is
XX possible to generate a variety of (nanoscale) protein structures, such as
XX assemblies in general, including matrix, filter, network, grid and
XX scaffold structures. Use of the protein structures in the purification of
XX biological fluids, for assembling cells for cell and tissue engineering,
XX and in surface engineering procedures is claimed.
XX
SQ Sequence 28 AA;

Query Match 64.4%; Score 85; DB 8; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.00011;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 KIAALKQKIASLKQIEDALEYENDALEQ 28
Db 1 KIRRLKQKIALKQIEIALAYETALAEQ 28

RESULT 7
AAB74345
ID AAB74345 standard; peptide; 28 AA.
XX
AC AAB74345;
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2A.
XX
KW Atomic Force Microscopy; AFM.
XX
OS Unidentified.

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XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2A
XX SQ Sequence 28 AA;

Query Match 62.1%; Score 82; DB 4; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.00029;
Matches 21; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
||:|||||
Db 1 KISALKKQNASLKQEIAALEQETAALEQ 28
|||||

RESULT 8
AAB74348
ID AAB74348 standard; peptide; 28 AA.
XX AC AAB74348;
XX DT 02-JUL-2001 (first entry)
XX DE Peptide SAF-p2D.
XX KW Atomic Force Microscopy; AFM.
XX OS Unidentified.
XX PN WO200121646-A1.
XX PD 29-MAR-2001.
XX PF 18-SEP-2000; 2000WO-GB003576.
XX PR 17-SEP-1999; 99GB-00022013.
XX PA (UYSU-) UNIV SUSSEX.
XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX PFPI; 2001-335468/35.
XX PT New protein structures with peptide monomer units, useful in Atomic Force
XX PT Microscopy, purifying biological fluids, promoting tissue repair and
XX PT tissue engineering, or constructing nanoscale molecular sieves.
XX PS Disclosure; Page 9; 45pp; English.
XX CC The present invention relates to a protein structure with several first
XX CC peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;

Query Match 57.6%; Score 76; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.002;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
||:|||||
Db 1 KIRALKAKNAHLKQEIATALEQETAALEQ 28
|||||

RESULT 10
AAB74352
ID AAB74352 standard; peptide; 28 AA.
XX AC AAB74352;
XX CC A peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;

Query Match 57.6%; Score 76; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.002;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALEYENDALEQ 28
||:|||||
Db 1 KIRALKAKNAHLKQEIATALEQETAALEQ 28
|||||

RESULT 10
AAB74352
ID AAB74352 standard; peptide; 28 AA.
XX AC AAB74352;
XX CC A peptide monomer units arranged in a first strand and several second
XX CC peptide monomer units arranged in a second strand. The structure is
XX CC useful in Atomic Force Microscopy and a number of other applications. The
XX CC present sequence is the peptide monomer unit SAF-p2D
XX SQ Sequence 28 AA;
```


DT 02-JUL-2001 (first entry)
 XX Peptide SAP-p2.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAP-p2
 XX Sequence 28 AA;
 SQ

Query Match 57.6%; Score 76; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.002; 8; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDALEYENDALEQ 28
 ||||| ||||| ||||| ||||| |||||
 DB 1 KIRALKKQNAHLKQEIATALEQEIATALEQ 28

RESULT 11
 AAB74346
 ID AAB74346 standard; peptide; 28 AA.
 AC AAB74346;
 XX 02-JUL-2001 (first entry)
 DT Peptide SAP-p2B.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAP-p2
 XX Sequence 28 AA;
 SQ

Query Match 56.8%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0027;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDALEYENDALEQ 28
 ||||| ||||| ||||| ||||| |||||
 DB 1 KIRALKKQNAHLKQEIATALEQEIATALEQ 28

RESULT 12
 AAB74347
 ID AAB74347 standard; peptide; 28 AA.
 AC AAB74347;
 XX 02-JUL-2001 (first entry)
 DT Peptide SAF-p2C.
 DE Atomic Force Microscopy; AFM.
 XX Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX 18-SEP-2000; 2000WO-GB003576.
 XX 17-SEP-1999; 99GB-00022013.
 XX (UYSU-) UNIV SUSSEX.
 XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX Claim 16; Page 26; 45pp; English.
 XX The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-p2C
 XX Sequence 28 AA;
 SQ

Query Match 56.8%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0027;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDALEYENDALEQ 28
 ||||| ||||| ||||| ||||| |||||
 DB 1 KIRALKKQNAHLKQEIATALEQEIATALEQ 28

```
RESULT 13
AAB74349
ID AAB74349 standard; peptide; 28 AA.
XX
XX AAB74349;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide SAF-p2E.
DE
XX
XX Atomic Force Microscopy; AFM.
KW
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 9; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2E
XX
XX Sequence 28 AA;
SQ
Query Match 56.1%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0037;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIRALKOKIASLKQETDALEYENDALEQ 28
DB 1 KIRALKOKIAHLKQETIAALEQETIAALEQ 28

RESULT 14
AAB74355
ID AAB74355 standard; peptide; 28 AA.
XX
XX AAB74355;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide used to form blunt-ended heterodimers.
DE
XX
XX Atomic Force Microscopy; AFM.
KW
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 9; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p2E
XX
XX Sequence 28 AA;
SQ
Query Match 53.0%; Score 70; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
DB 1 EIDALEYENDALEQ 14

RESULT 15
AAB74350
ID AAB74350 standard; peptide; 28 AA.
XX
XX AAB74350;
AC
XX
XX 02-JUL-2001 (first entry)
XX
XX Peptide SAF-p3.
DE
XX
XX Atomic Force Microscopy; AFM.
KW
XX
XX Unidentified.
OS
XX
XX WO200121646-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 18-SEP-2000; 2000WO-GB003576.
PF
XX
XX 17-SEP-1999; 99GB-00022013.
PR
XX
XX (UYSU-) UNIV SUSSEX.
PA
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
PI
XX WPI; 2001-335468/35.
DR
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
PT Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 12; 45pp; English.
PS
XX
XX The present invention relates to a protein structure with several first
CC peptide monomer units arranged in a first strand and several second
CC peptide monomer units arranged in a second strand. The structure is
CC useful in Atomic Force Microscopy and a number of other applications. The
CC present sequence is the peptide monomer unit SAF-p3
XX
XX Sequence 28 AA;
SQ
Query Match 53.0%; Score 70; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
| | | | | | | | | |
Db 1 EIDALEYENDALEQ 14

RESULT 16
ABR84737
ID ABR84737 standard; peptide; 28 AA.
XX
AC ABR84737;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX WO2003066660-A2.
PN
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001217.
XX
XX 05-FEB-2002; 2002US-0354376P.
PR
XX (IMMU-) IMMUNOLEX THERAPEUTICS APS.
PA
XX Caterer NR, Uttental LO, Neilson RW;
PI
XX WPI; 2003-679535/64.
DR
XX
XX Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
PT by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
XX Disclosure; Page 14; 35pp; English.
XX
XX The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 40.9%; Score 54; DB 7; Length 28;
Best Local Similarity 55.0%; Pred. No. 2.3;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDALE 20
| | | | | | | | | |
Db 5 KIAAIEBKIAIBETAAQE 24

RESULT 18
AAB50879
ID AAB50879 standard; peptide; 28 AA.
XX
AC AAB50879;
XX
DT 19-MAR-2001 (first entry)
XX
DE Integrin cytoplasmic domain heptad-repeat.
XX
KW Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin;
KW immunosuppressive; inflammatory bowel disease; arthritis;
KW multiple sclerosis; asthma; atherosclerosis; wound healing;
KW cytoplasmic domain; heptad-repeat.
XX
OS Homo sapiens.
XX
PN WO200073342-A1.
XX
PD 07-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US015153.
PF
XX 01-JUN-1999; 99US-00323447.
PR
XX (SCRI) SCRIPPS RES INST.
XX
XX Ginsberg MH, Pfaff M, Liu S;

Best Local Similarity 100.0%; Pred. No. 0.014; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIDALEYENDALEQ 28
| | | | | | | | | |
Db 1 EIDALEYENDALEQ 14

RESULT 16
ABR84737
ID ABR84737 standard; peptide; 28 AA.
XX
AC ABR84737;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #5.
XX
KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
KW AHEC; antiparallel; drug targeting.
XX
OS Synthetic.
XX WO2003066660-A2.
PN
XX
PD 14-AUG-2003.
XX
XX 05-FEB-2003; 2003WO-EP001217.
PF
XX 05-FEB-2002; 2002US-0354376P.
PR
XX (IMMU-) IMMUNOLEX THERAPEUTICS APS.
PA
XX Caterer NR, Uttental LO, Neilson RW;
PI
XX WPI; 2003-679535/64.
DR
XX
XX Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
PT by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX
XX Disclosure; Page 14; 35pp; English.
XX
XX The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention
XX
SQ Sequence 28 AA;

Query Match 43.2%; Score 57; DB 7; Length 28;
Best Local Similarity 60.0%; Pred. No. 0.88; Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDALE 20
| | | | | | | | | |
Db 5 KQAAIKNEIAIKQEIATIE 24

RESULT 17
ABR84736
ID ABR84736 standard; peptide; 28 AA.
XX
AC ABR84736;
XX
DT 18-DEC-2003 (first entry)
XX
DE DE novo designed AHEC peptide #4.

KW	infectious disease; food poisoning; Alzheimer's disease;
KW	amyloid beta-peptide; dental; MHC; major histocompatibility complex.
XX	Unidentified.
XX	WO2004087767-A1.
XX	14-OCT-2004.
XX	29-MAR-2004; 2004WO-JP004460.
XX	31-MAR-2003; 2003JP-00093243.
XX	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	Nishizawa T;
XX	WPI; 2004-737672/72.
XX	New polypeptide having a sequence in which an adhesion motif of a cell
XX	adhesion molecule is bonded to a polypeptide comprising a T cell epitope
XX	and a B cell epitope, and a linker peptide, useful for producing
XX	antibodies.
XX	Example 6; SEQ ID NO 22; 71pp; Japanese.
XX	The invention relates to a novel polypeptide capable of inducing the
XX	potentiation of antibody production when transmemorally having a sequence
XX	in which the amino acid sequence of an adhesion motif of a cell adhesion
XX	molecule is bonded to the polypeptide. The novel polypeptide comprises a
XX	peptide consisting of an amino acid sequence of a T cell epitope's amino
XX	terminal side and the amino acid sequence of a B cell epitope's carboxy
XX	terminal side and having a linker peptide between the amino acid
XX	sequences. The invention further comprises: novel DNA or RNA which
XX	encodes the polypeptide; microorganisms or animals and plants which have
XX	the DNA or RNA introduced; and a composition comprising the novel
XX	polypeptide and an additive for the formulation. The novel polypeptide
XX	has the following activities: antibacterial, neuroprotective, nootropic,
XX	and virucide. The novel polypeptide, encoding polynucleotide or
XX	composition are useful for producing antibodies in animals, for
XX	preventing or treating diseases. The novel polypeptide is useful as an
XX	adjuvant to increase the antibody production against antigenic proteins.
XX	The novel polypeptide is useful for producing an antibody against toxins
XX	of a pathogenic virus and microorganisms, thus effective in preventing or
XX	treating infectious disease such as food poisoning. The novel polypeptide
XX	is useful for treating Alzheimer's disease by producing an antibody
XX	against amyloid beta-peptide. The novel polypeptide is also useful for
XX	treating dental caries. This sequence represents a peptide relating to
XX	the antibody production of the invention.
XX	Sequence 28 AA;
XX	Query Match 31.1%; Score 41; DB 8; Length 28;
XX	Best Local Similarity 50.0%; Pred. No. 1.5e+02;
XX	Matches 12; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY	3 AALKOKIASLKOEDAL--EYEND 24
DB	4 AALKQYEADLKKTYEALKQYEAD 27
XX	RESULT 23
XX	AAR31981
XX	ID AAR31981 standard; peptide; 28 AA.
XX	AC AAR31981;
XX	AC AAR31981;
XX	25-MAR-2003 (revised)
XX	22-JUN-1993 (first entry)
XX	SSP7 polypeptide, suitable for in vivo expression.
XX	Heptad; plants; custom tailored storage proteins.

KW	1 KIAALKOKIASLKOEDALE 20
DB	4 KIKALEKLEKLEKLEKALE 23
XX	RESULT 21
XX	ABR84735
XX	ID ABR84735 standard; peptide; 28 AA.
XX	AC ABR84735;
XX	DT 18-DEC-2003 (first entry)
XX	DE novo designed AHEC peptide #3.
XX	Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
XX	AHEC; antiparallel; drug targeting.
XX	Synthetic.
XX	WO2003066660-A2.
XX	14-AUG-2003.
XX	05-FEB-2003; 2003WO-EP001217.
XX	05-FEB-2002; 2002US-0354376P.
XX	(IMMU-) IMMUNOLEX THERAPEUTICS APS.
XX	Caterer NR, Uttental LO, Neilson RW;
XX	WPI; 2003-679535/64.
XX	Composition useful for forming therapeutic antibodies and antibody
XX	fragments comprises pair of antibody Fv fragments linked and stabilized
XX	by antiparallel heterogeneous alpha-helical coiled-coil peptides.
XX	Disclosure; Page 14; 35pp; English.
XX	The present invention relates to a composition which comprises a pair of
XX	antibody Fv fragments linked and stabilised by antiparallel heterogeneous
XX	alpha-helical coiled-coil (AHEC) peptides. The composition is used to
XX	form multimeric complexes and therapeutic antibodies and antibody
XX	fragments useful for e.g. inhibition of receptor binding and the
XX	targeting of drugs, toxins and labels in research, industry and
XX	healthcare. The present sequence is an AHEC peptide used in the
XX	exemplification of the invention
XX	Sequence 28 AA;
XX	Query Match 34.1%; Score 45; DB 7; Length 28;
XX	Best Local Similarity 56.2%; Pred. NO. 41;
XX	Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY	1 KIAALKOKIASLKOEI 16
DB	12 BIAAIKDKIAAIKEI 27
XX	RESULT 22
XX	ADT02245
XX	ID ADT02245 standard; peptide; 28 AA.
XX	AC ADT02245;
XX	AC ADT02245;
XX	30-DEC-2004 (first entry)
XX	Surface protein antigen (Pac) peptide, SEQ ID 22.
XX	potentiation; antibody production; cell adhesion; T cell; B cell;
XX	epitope; antibacterial; neuroprotective; nootropic; virucide;

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XX OS Synthetic.
XX PN WO9303160-A1.
XX XX
XX PD 18-FEB-1993.
XX XX
XX PF 07-AUG-1992; 92WO-US006412.
XX PR 09-AUG-1991; 91US-00743006.
XX XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC, Keeler SJ, Rice JA;
XX XX WPI; 1993-076517/09.
XX DR
XX PT Synthetic polypeptide(s) contg. specified heptad units - expressed in
XX PT vivo in plants to serve as custom-tailored storage proteins with
XX PT specified aminoacid content.
XX XX
XX PS Claim 7; Page 103; 176pp; English.
XX CC The sequence represents a synthetic polypeptide comprising heptad units
XX CC of the peptide. The synthetic polypeptide can be expressed in vivo in
XX CC plants to serve as a synthetic seed storage protein which can be custom-
XX CC tailored for specific end-user requirements. The DNA encoding the heptad
XX CC may be used to transform plants to increase the content of partic. amino
XX CC acids such as lysine or methionine in seeds or leaves. See also AAR31979-
XX CC 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

OY 1 KIAALKQKIASLKQETDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 24
ADA15966
ID AAR78256 standard; peptide; 28 AA.
XX AC
XX AD A15966;
XX XX
XX DT 06-NOV-2003 (first entry)
XX DE
XX DE Synthetic storage protein, SSP, peptide SSP(7)4.
XX XX
XX KW lysC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase;
XX KW DHDPs; lysine inhibition; lysine ketoglutarate reductase; LKR;
XX KW chloroplast transit sequence; CTS; aspartokinase III; AKIII;
XX KW synthetic seed storage protein; SSP.
XX XX
XX OS Synthetic.
XX XX
XX PN US6459019-B1.
XX PD
XX PD 01-OCT-2002.
XX XX
XX PF 24-MAR-1997; 97US-00823771.
XX XX
XX PR 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX XX
XX PI Falco SC, Keeler SJ, Rice JA;
XX XX WPI; 2003-028272/02.
XX DR N-PSDB; ADA15964.
XX DR
XX XX Transformed plants that accumulate lysine at higher levels in its seeds
XX PT than untransformed plants, has gene fragments encoding lysine-insensitive
XX PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX XX
XX PS Example 21; Col 81; 109pp; English.
XX XX
XX CC The invention relates to a plant comprising two foreign nucleotide
XX CC sequences which cause seeds obtained from the plant to accumulate lysine
XX CC at a level of at least 10% higher than seeds of a plant that do not
XX CC comprise the nucleotide, where the nucleotide comprises a fragment
XX CC encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive
XX CC to lysine inhibition, and a fragment encoding a plant lysine

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XX XX New chimeric gene providing increased lysine content in plant seeds -
XX PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX PT transport sequence and seed specific promoter, also new plants of
XX PT improved nutritional value.
XX XX
XX PS Example 8; Page 81; 180pp; English.
XX XX
XX CC Oligonucleotide SM98 (AAQ95000) and complementary sequence SM99
XX CC (AAQ95001) code for 4 repeats (AAR78256) of heptad peptide SSP7 (see also
XX CC AAR78237). Clone 5-1 (AAQ95005) was obtd. by insertion of the
XX CC oligonucleotides into the Earl site of clone 84-H3 (see AAQ94993) and
XX CC transformation of Escherichia coli DH5 alpha. Synthetic storage protein
XX CC SSPs-1 (AAR78259) encoded by the construct can be used to raise the
XX CC lysine content in seeds of transformed plants
XX XX
XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

OY 1 KIAALKQKIASLKQETDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 25
ADA15966
ID ADA15966 standard; peptide; 28 AA.
XX AC
XX AD A15966;
XX XX
XX DT 06-NOV-2003 (first entry)
XX XX
XX DE Synthetic storage protein, SSP, peptide SSP(7)4.
XX XX
XX KW lysC; transgenic; lysine accumulation; dihydrodipicolinic acid synthase;
XX KW DHDPs; lysine inhibition; lysine ketoglutarate reductase; LKR;
XX KW chloroplast transit sequence; CTS; aspartokinase III; AKIII;
XX KW synthetic seed storage protein; SSP.
XX XX
XX OS Synthetic.
XX XX
XX PN US6459019-B1.
XX PD
XX PD 01-OCT-2002.
XX XX
XX PF 24-MAR-1997; 97US-00823771.
XX XX
XX PR 19-MAR-1992; 92US-00855414.
XX PR 06-JAN-1994; 94US-00178212.
XX PR 07-JUN-1995; 95US-00474633.
XX XX
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX XX
XX PI Falco SC, Keeler SJ, Rice JA;
XX XX WPI; 2003-028272/02.
XX DR N-PSDB; ADA15964.
XX DR
XX XX Transformed plants that accumulate lysine at higher levels in its seeds
XX PT than untransformed plants, has gene fragments encoding lysine-insensitive
XX PT dihydrodipicolinic acid synthase and lysine ketoglutarate reductase.
XX XX
XX PS Example 21; Col 81; 109pp; English.
XX XX
XX CC The invention relates to a plant comprising two foreign nucleotide
XX CC sequences which cause seeds obtained from the plant to accumulate lysine
XX CC at a level of at least 10% higher than seeds of a plant that do not
XX CC comprise the nucleotide, where the nucleotide comprises a fragment
XX CC encoding a dihydrodipicolinic acid synthase (DHDPs) that is insensitive
XX CC to lysine inhibition, and a fragment encoding a plant lysine

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CC ketoglutarate reductase (LKR) or its subfragment. The nucleotide fragment
 CC is operably linked to a plant chloroplast transit sequence (CTS) and the
 CC plant lysine ketoglutarate reductase subfragment is used in antisense
 CC inhibition or cosuppression. Also included are progeny plants from the
 CC above mentioned plant and seeds obtained from the above mentioned plant.
 CC The seeds obtained from the above mentioned plant (e.g., rapeseed,
 CC soybean or corn) comprising the foreign nucleic acid sequences accumulate
 CC lysine at a higher level, preferably at a level of at least 10% higher
 CC than seeds of a plant that do not comprise the foreign nucleic acid
 CC sequences. Chimaeric gene comprising DHDPS from *C. glutamicum* and
 CC aspartokinase III (from the *lysC* gene) of *E. coli* (mutated to be lysine-
 CC insensitive) are also used to generate the above transgenic plants. Also
 CC disclosed are synthetic seed storage proteins (SSP) used as an internal
 CC source of lysine, built up from synthetic peptide monomers based around
 CC an *Eari* site sequence (for generating multimeric proteins). The present
 CC sequence is an SSP peptide monomer.

XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 6; Length 28;
 Best Local Similarity 25.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQEIADALE 20
 Db 4 KLVKWEKLVKWEKLVKWE 23

RESULT 26

ID ABO44343 standard; peptide; 28 AA.

XX AC ABO44343;

XX DT 25-SEP-2003 (first entry)

XX DE Ear I-based lysine-rich heptad repeat SSP(7)4.

XX Aspartokinase; AKIIF; dihydrodipicolinic acid synthase; DHDPS;
 KW seed lysine content; seed threonine content; seed storage protein; SSP;
 KW chloroplast transit sequence; lysine-rich protein;
 KW lysine ketoglutarate reductase; LKR; transgenic.

XX OS Synthetic.

XX FN US2003056242-A1.

XX PD 20-MAR-2003.

XX PF 17-DEC-2001; 2001US-00023066.

XX PR 19-MAR-1992; 92US-00855414.

XX PR 18-MAR-1993; 93WO-US002480.

XX PR 06-JAN-1994; 94US-00178212.

XX PR 07-JUN-1995; 95US-00474633.

XX PR 24-MAR-1997; 97US-00823771.

XX FA (FALC/) FALCO S C.

XX PI Falco SC;

XX DR WPI; 2003-521869/49.

XX DR N-PSDB; ACH03709.

XX Example 21; Page 44; 116pp; English.

XX The invention relates to an isolated nucleic acid fragment comprising a
 CC first nucleic acid subfragment encoding aspartokinase (AK) that is
 CC substantially insensitive to inhibition by lysine, and a second nucleic

CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPS) that
 CC is substantially insensitive to inhibition by lysine. Also included are
 CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
 CC encoding lysine ketoglutarate reductase (LKR), a chimaeric gene (where
 CC the nucleic acid fragment is operably linked to a plant chloroplast
 CC transit sequence and to a seed-specific regulatory sequence, a plant
 CC comprising the nucleic acid/chimaeric gene in its genome, a seed obtained
 CC from the plant, increasing threonine or lysine content of the seeds of
 CC plant, a plant capable of transmitting the chimaeric gene to a progeny of
 CC plant having the ability to produce levels of free threonine or lysine at
 CC least two times greater than the free threonine levels of untransformed
 CC plants, a transformed (soybean) plant comprising seeds that accumulate
 CC lysine at a level at least ten percent to four-fold higher than the seeds
 CC of an untransformed plant, a transformed rapeseed comprising seeds that
 CC accumulate lysine to a level between ten percent and one hundred percent
 CC higher than that of the seeds of an untransformed plant, a monocot plant
 CC comprising in its genome the nucleic acid fragment having the monocot-
 CC embryo specific promoter and a transformed corn plant comprising seeds
 CC that accumulate lysine to a level between ten percent and one hundred
 CC thirty percent higher than the seeds of the untransformed plant. Also
 CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
 CC from monomer lysine-rich heptad repeats (encoded by *Eari* restriction
 CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
 CC plant. The nucleic acid fragments, genes and methods are useful for
 CC increasing threonine or lysine content of the seeds of the plant. Seeds
 CC containing increased threonine or lysine content eliminate the need to
 CC supplement mixed grain feeds with lysine or threonine produced via
 CC microbial fermentation. The present sequence is a lysine-rich heptad
 CC repeat for use as a monomer unit in a synthetic seed storage protein

XX SQ Sequence 28 AA;

Query Match 30.3%; Score 40; DB 6; Length 28;
 Best Local Similarity 25.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQEIADALE 20
 Db 4 KLVKWEKLVKWEKLVKWE 23

RESULT 27

ADW71693

ID ADW71693 standard; peptide; 28 AA.

XX AC ADW71693;

XX DT 24-MAR-2005 (first entry)

XX DE Peptide SSP(7)4 SEQ ID NO:70.

XX transgenic plant; amino acid production; seed; enzyme engineering.
 XX Synthetic.

XX OS US2005005330-A1.

XX PN 06-JAN-2005.

XX PD 19-MAR-2004; 2004US-00804678.

XX PF 06-JAN-1994; 94US-00178212.

XX PR 07-JUN-1995; 95US-00474633.

XX PR 27-MAR-1997; 97US-00824827.

XX PR 27-MAR-1998; 98US-00049304.

XX (FALC/) FALCO S C.

XX (MCDE/) MCDEVITT R E.

XX (EPEL/) EPELBAUM S U.

XX Falco SC, Mcdevitt RE, Epelbaum SU;

XX WPI; 2005-065280/07.

DR N-PSDB; ADW71691.
XX
XX New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PT seeds of transformed plants.
XX
XX Example 21; SEQ ID NO 70; 142pp; English.
XX
XX The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisease inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence represents a
CC peptide encoded by an oligonucleotide used to create chimeric genes of
XX the invention.
XX
SQ Sequence 28 AA;
Query Match 30.3%; Score 40; DB 9; Length 28;
Best Local Similarity 25.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
QY 1 KIAALKQKIASLKQETDALE 20
Db |:|::|:|::|:|::|:|
4 KLMKEEKLKAMEEKLKAME 23
RESULT 28
AAR76756
ID AAR76756 standard; peptide; 28 AA.
AC AAR76756;
XX
XX 18-MAR-1996 (first entry)
DT
DE E. coli FimH MFP class (+) binding peptide, sM5(28-54).
XX
XX FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue;
KW FimA; FimF; FimG; receptor binding site; MEP class; MF class; M class.
XX
XX Synthetic.
OS
XX WO9520657-A1.
PN
XX 03-AUG-1995.
PD
XX 27-JAN-1995; 95WO-DK000042.
PF
XX 27-JAN-1994; 94US-00187166.
PR
XX (GXBI-) GX BIOSYSTEMS AS.
PA
XX Sokurenko EV, Hasty DL, Klemm P, Pallesen L, Molin S;
PI WPI; 1995-275442/36.
XX
XX Receptor specific bacterial adhesins - useful for targeting active
PT compounds and microbial cells to locations of receptors.
PT
XX Example 4; Page 67; 152pp; English.
PS
XX The sequences given in AAR76749-62 represent peptide fragments which were
CC used in adhesion assays with the FimH protein from E. coli strain CGH-50
CC to test the binding of the MFP class of FimH adhesins. Most forms of the
CC FimH adhesin target, and bind to, oligosaccharide structures containing
CC terminally located alpha-D-mannoside residues. FimH contains 4 cysteine
CC residues assumed to direct folding of the molecule into distinct
CC functional domains. For comparison FimA and the minor components FimF and
CC FimG only have 2 cysteine residues. The localisation of the cysteine
CC residues in FimH points to a tandem arrangement of two ancestral genes.
CC Similar amino acids can be found in similar positions in the two halves
CC

CC of the FimH protein. The "midway" point is located roughly around residue
CC 150 in the mature protein. The two halves or domains of FimH have evolved
CC differently with the N-terminal section becoming the domain harbouring
CC the receptor binding site, whereas the C-terminal sector became the
CC domain of the molecule required for integration into the fimbrial
CC organelle. Variant FimH adhesins may be useful for targeting active
CC compounds and microbial cells to locations comprising selected receptors
CC to which the adhesins bind
XX
SQ Sequence 28 AA;
Query Match 28.8%; Score 38; DB 2; Length 28;
Best Local Similarity 40.9%; Pred. No. 3.9e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 6 KOKIASLKQETDALEEVENDALE 27
Db |:|::|:|::|:|::|:|
1 KTKNEGLKTENEGSLKTENEGLK 22
RESULT 29
AAR32693
ID AAR32693 standard; protein; 28 AA.
XX
XX AAR32693;
AC
XX 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
DT
XX
DE SSP polypeptide produced from clone 84-H3.
XX
XX Heptad; plants; custom tailored storage proteins; in vivo; expression.
KW
XX Synthetic.
OS
XX WO9303160-A1.
PN
XX 18-FEB-1993.
PD
XX 07-AUG-1992; 92WO-US006412.
PF
XX 09-AUG-1991; 91US-00743006.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA
XX Falco SC, Keeler SJ, Rice JA;
PI WPI; 1993-076517/09.
XX
XX N-PSDB; AAQ37274.
DR
XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
XX Disclosure; Page 124; 176pp; English.
PS
XX The sequence represents a synthetic heptad polypeptide which can be
CC expressed in vivo in plants to serve as a synthetic seed storage protein
CC which can be custom-tailored for specific end-user requirements. The DNA
CC encoding the heptad may be used to transform plants to increase the
CC content of partic. amino acids such as lysine or methionine in seeds or
CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
CC MAR-2003 to correct FN field.)
XX
SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
QY 1 KIAALKQKIASLKQETDALE 20
Db |:|::|:|::|:|::|:|
4 KMKAMEEKLKAMEEKLKAME 23

RESULT 30
AAR32689
ID AAR32689 standard; peptide; 28 AA.

XX AC AAR32689;
XX 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX XX
XX SSP polypeptide produced from clone D16.

XX Heptad; plants; custom tailored storage proteins; in vivo; expression.
XX OS
XX Synthetic.

XX WO9303160-A1.

XX 18-FEB-1993.

XX 07-AUG-1992; 92WO-US006412.

XX 09-AUG-1991; 91US-00743006.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1993-076517/09.

XX N-FSDB; AAQ3270.

XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.

XX Disclosure; Page 120; 176pp; English.

XX The sequence represents a synthetic heptad polypeptide which can be
CC expressed in vivo in plants to serve as a synthetic seed storage protein
CC which can be custom-tailored for specific end-user requirements. The DNA
CC encoding the heptad may be used to transform plants to increase the
CC content of partic. amino acids such as lysine or methionine in seeds or
CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
CC MAR-2003 to correct PN field.)

XX SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQEIADALE 20

Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 31

AAR31980
ID AAR31980 standard; peptide; 28 AA.

XX AAR31980;

XX 25-MAR-2003 (revised)

DT 22-JUN-1993 (first entry)

XX SSP5 polypeptide, suitable for in vivo expression.

XX Heptad; plants; custom tailored storage proteins.

XX Synthetic.

XX WO9303160-A1.

New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of

XX 18-FEB-1993.
XX 07-AUG-1992; 92WO-US006412.
XX 09-AUG-1991; 91US-00743006.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Keeler SJ, Rice JA;
XX WPI; 1993-076517/09.
XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX Claim 7; Page 102; 176pp; English.
XX The sequence represents a synthetic polypeptide comprising heptad units
CC of the peptide. The synthetic polypeptide can be expressed in vivo in
CC plants to serve as a synthetic seed storage protein which can be custom-
CC tailored for specific end-user requirements. The DNA encoding the heptad
CC may be used to transform plants to increase the content of partic. amino
CC acids such as lysine or methionine in seeds or leaves. See also AAR31979-
CC 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKQEIADALE 20

Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 32

AAR78255
ID AAR78255 standard; peptide; 28 AA.

XX AAR78255;

DT 15-JUL-1996 (first entry)

XX SSP(S)4 heptad.

XX Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.

XX Synthetic.

XX WO9515392-A1.

XX 08-JUN-1995.

XX 21-NOV-1994; 94WO-US013190.

XX 30-NOV-1993; 93US-00160117.

XX 17-JUN-1994; 94US-00261661.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1995-215272/28.

XX N-FSDB; AAQ94998.

```

PT improved nutritional value.
PS Example 8; Page 81; 180pp; English.
XX
CC Oligonucleotide SM96 (AAQ94998) and complementary sequence SM97
CC (AAQ94999) code for 4 repeats (AAR78255) of heptad peptide SSP5 (see also
CC AAR78238). Clone 3-5 (AAQ95006) was obtd. by insertion of the first 22
CC bases of the SM96-SM97 set into the EarI site of clone 82-4 (see
CC AAQ94992) and transformation of Escherichia coli DH5 alpha. Synthetic
CC storage protein SSP3-5 (AAR78260) encoded by the construct was used to
CC raise the lysine content in seeds of transformed tobacco, soybean and
CC corn
XX
SQ Sequence 28 AA;
    Query Match      28.0%; Score 37; DB 2; Length 28;
    Best Local Similarity 25.0%; Pred. No. 5.4e+02;
    Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI DALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 33
AAR78250
ID AAR78250 standard; protein; 28 AA.
XX
AC AAR78250;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..7 /label= SSP5
FT Peptide 8..14 /label= SSP5
FT Peptide 15..21 /label= SSP5
FT Peptide 22..28 /label= SSP5
FT Peptide
XX
PN WO9515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
DR N-PSDB; AAQ94993.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 136; 180pp; English.
XX

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CC Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78250) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obtd. by insertion of HPLC-purified SSP5
CC -encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the
CC resulting vector to transform Escherichia coli JM103, yielding clone 84-
CC H3 (AAQ94993). The SSP forms a coiled-coil structure. It can be expressed
CC in the seeds of transformed plants, e.g. soybean and corn, to increase
CC lysine content
XX
SQ Sequence 28 AA;
    Query Match      28.0%; Score 37; DB 2; Length 28;
    Best Local Similarity 25.0%; Pred. No. 5.4e+02;
    Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI DALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 34
AAR78244
ID AAR78244 standard; protein; 28 AA.
XX
AC AAR78244;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..7 /label= SSP5
FT Peptide 8..14 /label= SSP5
FT Peptide 15..21 /label= SSP5
FT Peptide 22..28 /label= SSP5
FT Peptide
XX
PN WO9515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
DR N-PSDB; AAQ94983.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 129; 180pp; English.
XX

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CC Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78244) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obtd. by insertion of SSP5-encoding
CC oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector

```

CC to transform *Escherichia coli* JM103, yielding clone D33 (AAQ94983). The
 CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
 CC transformed plants, e.g. soybean and corn, to increase lysine content
 XX
 SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
 Best Local Similarity 25.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIADALE 20
 ID AAW62935 standard; peptide; 28 AA.
 DB 4 KMKAMEEKMKAMEEKMKAME 23
 AC AAW62935;
 XX
 XX
 DT 02-OCT-1998 (first entry)
 XX
 DE Minimalist lytic peptide.
 XX
 XX
 KW Lytic peptide; channel forming peptide; antibacterial; amphipathic.
 XX
 OS Synthetic.
 XX
 PN US5789542-A.
 XX
 PD 04-AUG-1998.
 XX
 PF 06-OCT-1997; 97US-00944133.
 XX
 PR 22-APR-1994; 94US-00232525.
 PR 22-JUL-1996; 96US-00681075.
 PR 03-FEB-1997; 97US-00789077.
 XX
 XX (LOU) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
 XX
 XX Becker CL, McLaughlin ML;
 WPI; 1998-446183/38.
 XX
 XX Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
 mer lytic peptides.
 FT
 FT Disclosure; Col 5; 25pp; English.
 PS
 XX
 CC AAW62920-67 represent minimalist lytic (channel forming) peptides. The
 CC peptides have antibacterial properties in concentrations not lethal
 CC toward mammalian cells. The peptides are heptads (or heptad multimers)
 CC that comprise four nonpolar amino acid residues and three positively
 CC charged amino acid residues, or five nonpolar amino acid residues and two
 CC positively charged amino acid residues. The nonpolar amino acid residues
 CC and the positively charged amino acid residues are distributed within the
 CC heptad such that when the multimer forms an alpha-helix the nonpolar
 CC amino acid residues will lie on one face of the alpha-helix, and the
 CC positively charged amino acid residues will lie on the opposite face of
 CC the alpha-helix, whereby the multimer is amphipathic
 XX
 SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
 Best Local Similarity 34.6%; Pred. No. 9.4e+02;
 Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQEIADALEYENDALE 27
 DB 3 LKALKKALKKALKKALKKALKKALK 28
 AC

RESULT 37
 AAW62947
 ID AAW62947 standard; peptide; 28 AA.
 XX
 AC AAW62947;

CC to transform *Escherichia coli* JM103, yielding clone D33 (AAQ94983). The
 CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
 CC transformed plants, e.g. soybean and corn, to increase lysine content
 XX
 SQ Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
 Best Local Similarity 25.0%; Pred. No. 5.4e+02;
 Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIADALE 20
 ID AAW62935 standard; protein; 28 AA.
 DB 4 KMKAMEEKMKAMEEKMKAME 23
 AC AAR78242;
 XX
 XX
 DT 15-JUL-1996 (first entry)
 XX
 DE SSP 5.5.5.5.
 XX
 KW Lysine; synthetic storage protein; SSP; vector; pSK6;
 KW dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
 KW Glycine max; transgenic plant; essential amino acid.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..7
 FT /label= SSP5
 FT Peptide 8..14
 FT /label= SSP5
 FT Peptide 15..21
 FT /label= SSP5
 FT Peptide 22..28
 FT /label= SSP5
 XX
 XX WO9515392-A1.
 XX
 PD 08-JUN-1995.
 XX
 XX 21-NOV-1994; 94WO-US013190.
 XX
 PR 30-NOV-1993; 93US-00160117.
 PR 17-JUN-1994; 94US-00261661.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Falco SC, Keeler SJ, Rice JA;
 PI
 XX WPI; 1995-215272/28.
 DR
 XX N-ESDB; AAQ94981.
 XX
 XX New chimeric gene providing increased lysine content in plant seeds -
 PT contains dihydrodipicolinic acid synthase gene coupled to chloroplast
 PT transport sequence and seed specific promoter, also new plants of
 PT improved nutritional value.
 XX
 XX Example 8; Page 127; 180pp; English.
 PS
 XX Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78242) comprises 2
 CC heptad SSPs repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
 CC derived from vector pSK6. It was obtd. by insertion of SSP5-encoding
 CC oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector
 CC to transform *Escherichia coli* JM103, yielding clone D16 (AAQ94981). The
 CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
 CC transformed plants, e.g. soybean and corn, to increase lysine content
 XX
 XX Sequence 28 AA;

```

XX DT 02-OCT-1998 (first entry)
XX DE Minimalist lytic peptide.
XX KW Lytic peptide; channel forming peptide; antibacterial; amphipathic.
XX OS Synthetic.
XX PN US5789542-A.
XX PD 04-AUG-1998.
XX PF 06-OCT-1997; 97US-00944133.
XX PR 22-APR-1994; 94US-00232525.
XX PR 22-JUL-1996; 96US-00681075.
XX PR 03-FEB-1997; 97US-00789077.
XX (LOU ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.
XX PA Becker CL, McLaughlin ML;
XX PI WPI; 1998-446183/38.
XX DR Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
XX PT mer lytic peptides.
XX PS Disclosure; Col 6; 25pp; English.
XX CC AAW62920-67 represent minimalist lytic (channel forming) peptides. The
XX CC peptides have antibacterial properties in concentrations not lethal
XX CC toward mammalian cells. The peptides are heptads (or heptad multimers)
XX CC that comprise four nonpolar amino acid residues and three positively
XX CC charged amino acid residues, or five nonpolar amino acid residues and two
XX CC positively charged amino acid residues. The nonpolar amino acid residues
XX CC and the positively charged amino acid residues are distributed within the
XX CC heptad such that when the multimer forms an alpha-helix the nonpolar
XX CC amino acid residues will lie on one face of the alpha-helix, and the
XX CC positively charged amino acid residues will lie on the opposite face of
XX CC the alpha-helix, whereby the multimer is amphipathic
XX SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 36.0%; Pred. No. 5.4e+02;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 ALKQKTASLKQETDALEYENDALEQ 28
| | | : : | | : | | : | | :
Db 2 ALKALKALKALKALKALKALKKK 26

RESULT 38
AAW60508
ID AAW60508 standard; protein; 28 AA.
XX AC AAW60508;
XX DT 25-MAR-2003 (revised)
XX DT 25-AUG-1998 (first entry)
XX Synthetic storage protein of the specification.
XX KW Dihydrodipicolinic acid synthase; DHDPs; chimeric gene; storage protein;
XX KW lysine inhibition; plant chloroplast transit sequence;
XX KW plant seed-specific regulatory sequence; transgenic plant;
XX KW increased lysine level; corn; Zea mays; soybean; Glycine max.
XX OS Synthetic.
XX PN US5773691-A.
XX

XX DT 30-JUN-1998.
XX PF 07-JUN-1995; 95US-00474633.
XX PR 19-MAR-1992; 92US-00855414.
XX PR 18-MAR-1993; 93WO-US002480.
XX PR 06-JAN-1994; 94US-00178212.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Falco SC;
XX XX WPI; 1998-387117/33.
XX Chimeric genes encoding lysine production enzymes - useful for increasing
XX PT transgenic seed lysine content without being inhibited by high levels of
XX PT the amino acid.
XX PS Example 21; Col 113-114; 106pp; English.
XX CC The present sequence represents a synthetic lysine rich, storage protein
XX CC of the specification. The sequence can be operably linked to a seed-
XX CC specific regulatory sequence to create a chimeric gene of the
XX CC specification. The specification also describes a Corynebacterium dapsa
XX CC gene, which encodes a dihydrodipicolinic acid synthase (DHDPs) enzyme,
XX CC which was used to create chimeric genes of the invention. The chimeric
XX CC genes contain a nucleic acid fragment encoding a DHDPs enzyme which is
XX CC insensitive to inhibition by lysine operably linked to a plant
XX CC chloroplast transit sequence and to a plant seed-specific regulatory
XX CC sequence. The chimeric genes are useful for producing plants containing
XX CC increased levels of lysine, especially in corn (Zea mays) and soybean
XX CC (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX SQ Sequence 28 AA;
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAALKQKTASLKQETDALE 20
| | : | | : | | : | | :
Db 4 KMKAMEEKMKAMEEKMAE 23

RESULT 39
AAW60516
ID AAW60516 standard; protein; 28 AA.
XX AC AAW60516;
XX DT 25-MAR-2003 (revised)
XX DT 25-AUG-1998 (first entry)
XX Synthetic storage protein of the specification.
XX KW Dihydrodipicolinic acid synthase; DHDPs; chimeric gene; storage protein;
XX KW lysine inhibition; plant chloroplast transit sequence;
XX KW plant seed-specific regulatory sequence; transgenic plant;
XX KW increased lysine level; corn; Zea mays; soybean; Glycine max.
XX OS Synthetic.
XX PN US5773691-A.
XX PD 30-JUN-1998.
XX PF 07-JUN-1995; 95US-00474633.
XX PR 19-MAR-1992; 92US-00855414.
XX PR 18-MAR-1993; 93WO-US002480.
XX PR 06-JAN-1994; 94US-00178212.
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.

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XX PI Falco SC;
XX WPI; 1998-387117/33.
XX N-PSDB; AAV35831.
XX Chimeric genes encoding lysine production enzymes - useful for increasing
XX transgenic seed lysine content without being inhibited by high levels of
XX the amino acid.
XX Example 21; Col 125-126; 106pp; English.
XX The present sequence represents a synthetic lysine rich, storage protein
XX of the specification. The sequence can be operably linked to a seed-
XX specific regulatory sequence to create a chimeric gene of the
XX specification. The specification also describes a Corynebacterium dapt
XX gene, which encodes a dihydrodipicolinic acid synthase (DHDPs) enzyme,
XX which was used to create chimeric genes of the invention. The chimeric
XX genes contain a nucleic acid fragment encoding a DHDPs enzyme which is
XX insensitive to inhibition by lysine operably linked to a plant
XX chloroplast transit sequence and to a plant seed-specific regulatory
XX sequence. The chimeric genes are useful for producing plants containing
XX increased levels of lysine, especially in corn (Zea mays) and soybean
XX (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLQKQIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 40
AAW60510
ID AAW60510 standard; protein; 28 AA.
AC AAW60510;
XX 25-MAR-2003 (revised)
XX 25-AUG-1998 (first entry)
XX Synthetic storage protein of the specification.
XX Dihydrodipicolinic acid synthase; DHDPs; chimeric gene; storage protein;
XX lysine inhibition; plant chloroplast transit sequence;
XX plant seed-specific regulatory sequence; transgenic plant;
XX increased lysine level; corn; Zea mays; soybean; Glycine max.
XX Synthetic.
XX OS
XX US5773691-A.
XX 30-JUN-1998.
XX 07-JUN-1995; 95US-00474633.
XX 19-MAR-1992; 92US-00855414.
XX 18-MAR-1993; 93WO-US002480.
XX 06-JAN-1994; 94US-00178212.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Falco SC;
XX WPI; 1998-387117/33.
XX Chimeric genes encoding lysine production enzymes - useful for increasing
XX transgenic seed lysine content without being inhibited by high levels of
XX the amino acid.

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XX Example 21; Col 115-116; 106pp; English.
XX The present sequence represents a synthetic lysine rich, storage protein
XX of the specification. The sequence can be operably linked to a seed-
XX specific regulatory sequence to create a chimeric gene of the
XX specification. The specification also describes a Corynebacterium dapt
XX gene, which encodes a dihydrodipicolinic acid synthase (DHDPs) enzyme,
XX which was used to create chimeric genes of the invention. The chimeric
XX genes contain a nucleic acid fragment encoding a DHDPs enzyme which is
XX insensitive to inhibition by lysine operably linked to a plant
XX chloroplast transit sequence and to a plant seed-specific regulatory
XX sequence. The chimeric genes are useful for producing plants containing
XX increased levels of lysine, especially in corn (Zea mays) and soybean
XX (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX Sequence 28 AA;

Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLQKQIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 41
AAW87744
ID AAW87744 standard; protein; 28 AA.
AC AAW87744;
XX 29-MAR-1999 (first entry)
XX Synthetic lysine-rich storage protein 5.5.5.5.
XX Lysine; transgenic plant; seed storage protein.
XX Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..7
XX /label= SSP5
XX Peptide 8..14
XX /label= SSP5
XX Peptide 15..21
XX /label= SSP5
XX Peptide 22..28
XX /label= SSP5
XX WO9842831-A2.
XX 01-OCT-1998.
XX 27-MAR-1998; 98WO-US006051.
XX 27-MAR-1997; 97US-00824627.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Falco SC, Mcdevitt RE, Epelbaum SU;
XX WPI; 1999-045139/04.
XX N-PSDB; AAV99516.
XX Nucleic acids and chimeric genes for increasing seed lysine content -
XX comprise sequence encoding all or part of lysine ketoglutarate reductase,
XX useful to improve nutritional quality of seeds from transformed plants.
XX Example 21; Page 137; 231pp; English.
XX This is the amino acid sequence of a lysine-rich synthetic seed storage

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1 KIAALKOKIASLKQEIADALE 20
 |:|::||:|::|:
 4 KMKAMEEKWKAMEEKWANE 23

RESULT 44
 ID AAE11041 standard; peptide; 28 AA.
 AC AAE11041;
 XX 18-DEC-2001 (first entry)
 XX Leucine zipper peptide #3.
 KW Tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 KW melanoma; leucine zipper peptide.
 OS Unidentified.
 OS US6284236-B1.
 PN 04-SEP-2001.
 PD 26-MAY-1999; 99US-00320424.
 PF 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 PR 25-JUN-1996; 96US-00670354.
 PR 26-MAR-1998; 98US-00048641.
 PR 10-NOV-1998; 98US-00190046.
 XX (IMMV) IMMUNEX CORP.
 XX Wiley SR, Goodwin RG;
 XX WPI; 2001-595463/67.
 DR New tumor necrosis factor related apoptosis inducing ligand polypeptides
 PPT for treating viral infections (e.g. bovine viral diarrhoea or human
 PPT immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).
 XX Claim 11; Col 14; 4lpp; English.
 XX The invention relates to a cytokine designated as tumour necrosis factor
 CC (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis
 CC of certain target cells, including cancer cells and virally infected
 CC cells. The TRAIL polypeptides are useful in killing cancer cells, in
 CC treating viral infections (e.g. bovine viral diarrhoea or human
 CC immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and
 CC melanoma), as a research reagent useful in studying apoptosis including
 CC the regulation of programmed cell death. TRAIL DNA sequences may be
 CC employed in developing a gene therapy approach to treating disorders
 CC mediated by defective or insufficient amounts of TRAIL, in the production
 CC of TRAIL polypeptides and as probes or primers in polymerase chain
 CC reactions (PCR). The present sequence is a leucine zipper peptide that
 CC promotes the trimerisation of TRAIL protein. The resulting trimeric TRAIL
 CC protein has enhanced biological activity
 XX Sequence 28 AA;

Query Match	28.0%;	Score 37;	DB 4;	Length 28;
Best Local Similarity	50.0%;	Pred. No.	5.4e+02;	
Matches	6;	Conservative	6;	Mismatches 0;
			Indels	0;
			Gaps	0;

9 IASIKORIDALE 20

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:36:04 ; Search time 23.5 Seconds
(without alignments)
114.641 Million cell updates/sec

Title: US-10-088-417a-1

Perfect score: 132

Sequence: 1 KIAALKQKIASLKQIDALEYENDALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 199

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	20.5	28	A61417	bdellin B-3 - medi
2	25	18.9	28	PL0005	pepsin A (EC 3.4.2
3	24	18.2	28	A44877	cell surface prote
4	22	16.7	28	S64701	hypothetical prote
5	21	15.9	28	B60071	vasoactive intesti
6	21	15.9	28	A60304	vasoactive intesti
7	21	15.9	28	G69384	conserved hypothet
8	20	15.2	28	PC1162	cytochrome-c oxida
9	20	15.2	28	A60303	vasoactive intesti
10	20	15.2	28	S21742	3-oxoacyl-[acyl-ca
11	20	15.2	28	T06340	ribosomal protein
12	19.5	14.8	28	H85908	hypothetical prote
13	19	14.4	28	A32643	deoxyribodipyrimid
14	19	14.4	28	S11618	ribosomal protein
15	19	14.4	28	JW0019	mast cell degranul
16	18.5	14.0	28	I48178	orphan receptor -
17	18	13.6	28	A34244	hexokinase (EC 2.7
18	18	13.6	28	A60752	outer membrane pro
19	18	13.6	28	S07826	venom protein - Am
20	18	13.6	28	S63502	95K protein - Euba
21	18	13.6	28	S16228	aryl acylamidase -
22	17	12.9	28	S66436	allophycocyanin al
23	17	12.9	28	S47624	D-aspartate oxidase
24	17	12.9	28	JX0059	serine proteinase
25	17	12.9	28	A38232	vasoactive intesti
26	17	12.9	28	S72460	ribosomal protein
27	17	12.9	28	A23691	apolipoprotein C-I
28	17	12.9	28	S56746	alpha-synuclein, N
29	17	12.9	28	S38524	rRNA N-glycosidase

30 17 12.9 28 2 PC4430 peroxisome prolife
31 17 12.9 28 2 PC4429 peroxisome prolife
32 17 12.9 28 2 A31859 deoxycytidine kina
33 16 12.1 28 2 T47196 RAS protein [impor
34 16 12.1 28 2 PH0231 T-cell receptor Vb
35 16 12.1 28 2 D49829 T-cell receptor va
36 16 12.1 28 2 S37683 protein IEF SSP 91
37 16 12.1 28 2 PS0106 2-phosphinomethylm
38 16 12.1 28 2 A69259 hypochetrical prote
39 16 12.1 28 2 T09594 gene LFY protein -
40 16 12.1 28 4 I68614 frame shifted FWR1
41 15 11.4 28 2 T12301 NADH2 dehydrogenas
42 15 11.4 28 2 A60291 24K proteinase (EC
43 15 11.4 28 2 S55729 orotidine-5'-monop
44 15 11.4 28 2 JX0058 trypsin inhibitor
45 15 11.4 28 2

ALIGNMENTS

RESULT 1

A61417
bdellin B-3 - medicinal leech (fragment)
C:Species: Hirudo medicinalis (medicinal leech)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 07-May-1999
C:Accession: A61417

R:Krejci, K.; Fritz, H.

FEBS Lett. 64, 152-155, 1976

A:Title: Structural homology of a trypsin-plasmin inhibitor from leeches (bdellin B-3) w
A:Reference number: A61417; MUID:76188026; PMID:131707

A:Accession: A61417

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-28 <KR>

A:CROSS-references: UNIPARC:UPI0000017BD89

Query Match 20.5%; Score 27; DB 2; Length 28;

Best Local Similarity 40.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 17 DALEYENDAL 26

Db 17 DGVTYDNECL 26

RESULT 2

PL0005

pepsin A (EC 3.4.23.1) precursor - Mongolian sheep (fragments)

C:Species: Ovis platyura (Mongolian sheep)

C>Date: 30-Jun-1992 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001

C:Accession: PL0005

R:Baudys, M.; Erdene, T.G.; Kostka, V.; Pavlik, M.; Foltmann, B.

Comp. Biochem. Physiol. B 89, 385-391, 1988

A:Title: Comparison between prothymosin and pepsinogen from lamb and calf.

A:Reference number: PL0006; MUID:88185059; PMID:3128424

A:Accession: PL0005

A:Molecule type: protein

A:Residues: 1-15;16-28 <BAU>

A:CROSS-references: UNIPARC:UPI0000017C5AD; UNIPARC:UPI0000017C5AE

A:Experimental source: stomach

C:Keywords: aspartic proteinase; hydrolase; protein digestion; zymogen

F:1-15/Domain: activation peptide (fragment) #status predicted <ACP>

Query Match 18.9%; Score 25; DB 2; Length 28;

Best Local Similarity 47.1%; Pred. No. 6.5e+03;

Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 1 KIAALKQKIASLKQKQK 17

Db 4 KIPLVKKK--SLRQVSD 18

```
RESULT 3
A44877
cell surface protein 2F5 91K component - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44877
R:Nardi, J.B.
Dev. Biol. 152, 161-171, 1992
A:Title: Dynamic expression of a cell surface protein during rearrangement of epithelial
A:Reference number: A44877; MUID:92331807; PMID:1628754
A:Accession: A44877
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-28 <NAR>
A:Cross-references: UNIPROT:Q9TWX0; UNIPARC:UPI000007FF81
A>Note: sequence extracted from NCBI backbone (NCBIP:108784)

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.6e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 12 LKQEIDALEVEN 23
DB 14 VKEQIESFEVIN 25

RESULT 4
S64701
hypothetical protein (aph1 5'-region) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S64701
R:Huang, Y.; Garrison, P.N.; Barnes, L.D.
Biochem. J. 312, 925-932, 1995
A:Title: Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5',5'-P(1)
n family.
A:Reference number: S64700; MUID:96128081; PMID:8554540
A:Accession: S64701
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-28 <HUA>
A:Cross-references: UNIPARC:UPI000017B1D8; EMBL:U32615

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.5e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQEIDALEY 21
DB 16 AEFNQQLRFLOQ 27

RESULT 5
B60071
vasoactive intestinal peptide - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998
C:Accession: B60071
R:Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
Regul. Pept. 32, 39-45, 1991
A:Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
A:Reference number: A60071; MUID:91164506; PMID:2003150
A:Accession: B60071
A>Status: protein sequence not shown
A:Molecule type: protein
A:Residues: 1-28 <YUA>
A:Cross-references: UNIPARC:UPI000002D1C0
A>Note: the sequence is identical with the human sequence
C:Superfamily: Glucagon
C:Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 QEIDALEYEND 24
DB 18 QKVDLREGERE 28

RESULT 8
PC1162
cytochrome-c oxidase (EC 1.9.3.1) chain III - goldfish mitochondrion (fragment)
C:Species: mitochondrion Carassius auratus (goldfish)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PC1162
R:Peng, G.; Taylor, J.D.; Tchen, T.T.
Biochem. Biophys. Res. Commun. 189, 445-449, 1992
A:Title: Increased mitochondrial activities in pigmented (melanized) fish cells and nuclei
A:Reference number: JCI348; MUID:93080595; PMID:1280425
```

```
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEIDALEYENDAL 26
DB 4 AVFTDNYTLRKQMAVKYLSIL 27

RESULT 6
A60304
vasoactive intestinal peptide - dog
N:Alternate names: VIP
C:Species: Canis lupus familiaris (dog)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
C:Accession: A60304
R:Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.
Regul. Pept. Suppl. 3, S14, 1985
A:Title: Purification and sequencing of dog and guinea pig VIP's.
A:Reference number: A60304
A:Accession: A60304
A:Molecule type: protein
A:Residues: 1-28 <ENG>
A:Cross-references: UNIPROT:P04565; UNIPARC:UPI000002D1C0
C:Superfamily: glucagon
C:Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 20.8%; Pred. No. 2e+04;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEIDALEYENDAL 26
DB 4 AVFTDNYTLRKQMAVKYLSIL 27

RESULT 7
G69384
conserved hypothetical protein AFI079 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69384
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sulton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69384
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-28 <KLE>
A:Cross-references: UNIPROT:O29184; UNIPARC:UPI0000056E69; GB:AE001028; GB:AE000782; NID:

Query Match 15.9%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 14 QEIDALEYEND 24
DB 18 QKVDLREGERE 28

RESULT 8
PC1162
cytochrome-c oxidase (EC 1.9.3.1) chain III - goldfish mitochondrion (fragment)
C:Species: mitochondrion Carassius auratus (goldfish)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PC1162
R:Peng, G.; Taylor, J.D.; Tchen, T.T.
Biochem. Biophys. Res. Commun. 189, 445-449, 1992
A:Title: Increased mitochondrial activities in pigmented (melanized) fish cells and nuclei
A:Reference number: JCI348; MUID:93080595; PMID:1280425
```

A;Accession: PC1162
A;Molecule type: DNA
A;Residues: 1-28 <PNA>
A;Cross-references: UNIPROT:Q9PSI6, UNIPARC:UPI00000FC513
C;Genetics:
A;Gene: fme1-3
A;Genome: mitochondrion
A;Genetic code: SGCI
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 3: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 16 IDALEY 21
:|:|
Db 13 LOAMEY 18

RESULT 9

A60303

vasoactive intestinal peptide - smaller spotted catshark

C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C:Date: 10-Nov-1992 #sequence revision 10-Nov-1992 #text_change 09-Jul-2004

C:Accession: A60303; A60314; S07432

R:Dimaline, R.; Thwaites, D.T.; Young, J.; Lee, C.M.; Thorndyke, M.C.

Regul. Pept. 18, 356, 1987

A:Title: A novel family of VIP-like peptides from the dogfish Scyliorhinus canicula.

A:Reference number: A60303

A:Accession: A60303

A:Molecule type: protein

A:Residues: 1-28 <DI>

A:Cross-references: UNIPROT:P09685; UNIPARC:UPI000013884B

A>Note: This reference is an abstract

R:Dimaline, R.; Thorndyke, M.C.; Young, J.

Regul. Pept. 14, 1-10, 1986

A:Title: Isolation and partial sequence of elasmobranch VIP.

A:Reference number: A60314; MUID:86234323; PMID:13715063

A:Accession: A60314

A:Molecule type: protein

A:Residues: 1-10 <DI>

A:Cross-references: UNIPARC:UPI000017662D

R:Dimaline, R.; Young, J.; Thwaites, D.T.; Lee, C.M.; Thorndyke, M.C.

Ann. N. Y. Acad. Sci. 527, 621-623, 1988

A:Title: Amino acid sequence of a biologically active vasoactive intestinal peptide from

A:Reference number: S07432

Query Match 15.2%; Score 20; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+04;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASL 12
| | : | | |
Db 15 KOMAVKCYINSL 26

RESULT 10
 121742
 121742 [acyl-carrier-protein] reductase (EC 1.1.1.100) - rape
 C:Species: Brassica napus (rape)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
 C:Accession: 221742
 R:Sheldon, P.S.; Kekwick, R.G.O.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.
 Biochim. Biophys. Acta 1120, 151-159, 1992

A: Title: 3-Oxoacyl-[ACPL] reductase from oilseed rape (*Brassica napus*)
 A: Reference number: S21742; MUID:92223071; PMID:1562591
 A: Accession: S21742
 A: Status: preliminary
 A: Molecule type: protein
 A: Residues: 1-28 <SHE>
 A: Cross-references: UNIPARC:UPI000017B028
 C: Keywords: oxidoreductase

Query Match	15.2%	Score 20;	DB 2;	Length 28;
Best Local Similarity	60.0%;	Pred. No. 2.6e+04;		
Matches	3: Conservative	2: Mismatches	0: Indels	0: Gaps

QY 17 DALEY 21
||:|
pb 1 DAVDY 5

RESULT 11
T06340
ribosomal protein S16 - soybean chloroplast (fragment)
C:Species: Chloroplast Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #Ces
C:Accession: T06340
R:Nielsen, N.C.
submitted to the EMBL Data Library, May 1995
A:Reference number: Z15613
A:Accession: T06340
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-28 <NIE>
A:Cross-references: UNIPROT:Q12307; UNIPARC:UPI0000008B
A:Experimental source: cultivar Resnik; leaf.
C:Genetics:
A:Gene: rps16
A:Genome: chloroplast
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match	15.2%;	Score 20;	DB 2;	Length 28;
Best Local Similarity	42.9%;	Pred. No. 2.6e+04;		
Matches	6:	Conservative	1:	Mismatches 7: Indels 0: Gaps 0:

Qy	9	I	A	S	L	K	Q	E	I	D	A	L	E	Y	E	22
					:											
Db	4	I	E	S	L	O	S	M	F	D	L	E	E	R	E	17

RESULT 12
H85908
hypothetical protein z3917 [imported] - Escherichia coli (strain O157:H7, s
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85908
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouilis,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference: H85908
A:Accession: H85908
A:Status: Preliminary
A:Model: 1258
A:Proteins: 1258
A:Cross-references: UNIPROT:Q8X415; UNIPARC:UPI00000D0566
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 23917

```

Query Match      14.8%; Score 19.5; DB 2; Length 28;
Best Local Similarity 38.1%; Pred. No. 3e+04;
Matches 8; Conservative 1; Mismatches 9; Indels 3; Gaps 1
QY      10 ASLKQETD---ALEYENDALE 27
      |||: ||| ||| |||

```

Db 7 APLQDAADLEIATEETSLE 27

RESULT 13

A32643
deoxyribipyrimidine photo-lyase (EC 4.1.1.99.3) - Methanobacterium thermoautotrophicum
N;Alternate names: photoreactivating enzyme
C;Species: Methanobacterium thermoautotrophicum
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Apr-1999
C;Accession: A32643
R;Kiener, A.; Hsain, I.; Sancar, A.; Walsh, C.
J. Biol. Chem. 264, 13880-13887, 1989
A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photolyase
A;Reference number: A32643; MUID:89340481; PMID:2668276
A;Accession: A32643
A;Molecule type: protein
A;Residues: 1-28 <KIE>
A;Cross-references: UNIPARC:UPI0000131976
C;Superfamily: deoxyribodipyrimidine photo-lyase
C;Keywords: carbon-carbon lyase; DNA binding

Query Match 14.4%; Score 19; DB 2; Length 28;

Best Local Similarity 44.4%; Pred. No. 3.5e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 QKTASLKQE 15

||| :|||

Db 5 ERIRSLNTE 13

RESULT 14

S11618
ribosomal protein S8 [validated] - Halobacterium salinarum (fragment)
N;Alternate names: ribosomal protein HS20
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S11618
R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea
A;Reference number: S11609
A;Accession: S11618
A;Molecule type: protein
A;Residues: 1-28 <YAG>
A;Cross-references: UNIPROT:Q7M552; UNIPARC:UPI0000177283
A;Note: the protein is designated as ribosomal protein HS20
A;Note: the source is designated as Halobacterium cutirubrum
C;Superfamily: Escherichia coli ribosomal protein S8
C;Keywords: protein biosynthesis; ribosome

Query Match 14.4%; Score 19; DB 2; Length 28;

Best Local Similarity 55.6%; Pred. No. 3.5e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 DALEYENDA 25

||| :|||

Db 8 DALSGIDDA 16

RESULT 15

JW0019
mast cell degranulating peptide - American common bumblebee
C;Species: Bombus pennsylvanicus (American common bumblebee)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JW0019
R;Argiolas, A.; Herring, P.; Pisano, J.J.
Peptides 6, 431-436, 1985
A;Title: Amino acid sequence of bumblebee MCD peptide: a new mast cell degranulating peptide
A;Reference number: JW0019; MUID:86177038; PMID:2421265
A;Accession: JW0019
A;Molecule type: protein
A;Residues: 1-28 <ARG>
A;Cross-references: UNIPROT:P04567; UNIPARC:UPI000012ED6C

A;Experimental source: venom

C;Keywords: amidated carboxyl end; venom

F;2-18,4-22/Disulfide bonds: #status experimental

F;28/Modified site: amidated carboxyl end (His) #status predicted

Query Match 14.4%; Score 19; DB 2; Length 28;

Best Local Similarity 30.8%; Pred. No. 3.5e+04;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQ 14

||| :|||

Db 14 ICKICRKICMMQ 26

RESULT 16

I48178
orphan receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I48178
R;Pena de Ortiz, S.; Cannon, M.M.; Jamieson, G.A.
Brain Res. Mol. Brain Res. 23, 278-283, 1994
A;Title: Expression of nuclear hormone receptors within the rat hippocampus: identification

A;Reference number: I48178; MUID:94335560; PMID:7914660

A;Accession: I48178

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: UNIPROT:Q63743; UNIPARC:UPI00000E8408; GB:L19344; NID:G349093; PIDN:?

Query Match 14.0%; Score 18.5; DB 2; Length 28;

Best Local Similarity 37.5%; Pred. No. 4e+04;
Matches 6; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 11 SLKQEID--ALEYEN 23

||| :|||

Db 6 SIQQNIQYKKLKNEN 21

RESULT 17

A34244
hexokinase (EC 2.7.1.1), pancreatic - rat (fragments)
N;Alternate names: glucokinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 03-Jun-1993 #text_change 28-Feb-1997
C;Accession: A34244
R;Magnuson, M.A.; Shelton, K.D.
J. Biol. Chem. 264, 15936-15942, 1989

A;Title: An alternate promoter in the glucokinase gene is active in the pancreatic beta cells

A;Reference number: A34244; MUID:89380186; PMID:2550428

A;Accession: A34244

A;Molecule type: mRNA

A;Residues: 1-28 <MAG>

A;Cross-references: UNIPARC:UPI000017553D; GB:M25807

A;Note: the authors translated the codon CTG for residue 2 as Lys

C;Superfamily: hexokinase; hexokinase homology

C;Keywords: ATP; glycolysis; phosphotransferase

Query Match 13.6%; Score 18; DB 2; Length 28;

Best Local Similarity 30.0%; Pred. No. 4.5e+04;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AALKQKIASL 12

||| :|||

Db 10 ATKKEKVEQI 19

RESULT 18

A60752
outer membrane protein A - Yersinia pseudotuberculosis (fragment)
N;Alternate names: heat-modifiable protein; outer membrane protein II
C;Species: Yersinia pseudotuberculosis
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004

C;Accession: A60752
R;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
J. Immunol. 143, 2955-2960, 1989
A;Title: The bacterial outer membrane protein that reacts with anti-HLA-B27 antibodies
A;Reference number: A60752; MUID:90038529; PMID:2478630
A;Accession: A60752
A;Molecule type: protein
A;Residues: 1-28 <ZHA>
A;Cross-references: UNIPROT:P38399; UNIPARC:UPI0000130CFC
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 4.5e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 20 EYEND 24
:|::|
Db 17 QYQDD 21

RESULT 19
S07826
venom protein - American tarantula (Eurytelma californica) (fragment)
C;Species: Eurytelma californica
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S07826
R;Savel-Niemann, A.
Biol. Chem. Hoppe-Seyler 370, 485-498, 1989
A;Title: Tarantula (Eurytelma californicum) venom, a multicomponent system.
A;Reference number: S04224; MUID:89302691; PMID:2742756
A;Accession: S07826
A;Molecule type: protein
A;Residues: 1-28 <SAV>
A;Cross-references: UNIPARC:UPI000017BE06
C;Keywords: venom

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 4.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AALKQKI 9
|:|
Db 10 AGVTQKI 16

RESULT 20
S63502
95K protein - Eubacterium acidaminophilum (fragment)
C;Species: Eubacterium acidaminophilum
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S63502
R;Meyer, M.; Granderath, K.; Andreessen, J.R.
Eur. J. Biochem. 234, 184-191, 1995
A;Title: Purification and characterization of protein P(B) of betaine reductase and its
phylum.

A;Reference number: S63502; MUID:96096737; PMID:8529639
A;Accession: S63502
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-28 <MEY>
A;Cross-references: UNIPROT:Q9R4G6; UNIPARC:UPI00000B2F3E

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 15 EIDALEYE 22
:|:|
Db 5 KIDGRELE 12

RESULT 21

S16228
aryl acylamidase - Nocardia globnerula
C;Species: Nocardia globnerula
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
A;Accession: S16228
R;Yoshioka, H.; Nagasawa, T.; Yamada, H.
Eur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globnerula.
A;Reference number: S16228; MUID:91293120; PMID:2065673
A;Accession: S16228
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <EUR>
A;Cross-references: UNIPROT:P80008; UNIPARC:UPI000001260D8

Query Match 13.6%; Score 18; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 16 IDALEY 21
:|:|
Db 1 MDVAEY 6

RESULT 22

S66436
allophycocyanin alpha-B chain - Anabaena sp. (strain PCC 7120) (fragment)
C;Species: Anabaena sp.
A;Variety: PCC 7120
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66436
R;Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
Eur. J. Biochem. 236, 1010-1024, 1996
A;Title: Isolation, characterization and electron microscopy analysis of a hemidiscoidal
A;Reference number: S66435; MUID:96270757; PMID:8665889
A;Accession: S66436
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DUC>
A;Cross-references: UNIPROT:P80556; UNIPARC:UPI00000174E0E
C;Superfamily: phycocyanin

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 14 QEIDALEY 21
|:|:|
Db 9 QADDELY 16

RESULT 23

S47624
D-aspartate oxidase (EC 1.4.3.1) - common octopus (fragment)
C;Species: Octopus vulgaris (common octopus)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 07-May-1999
C;Accession: S47624
R;Tedeschi, G.; Negri, A.; Cecilian, F.; Roñchi, S.; Vetere, A.; D'Aniello, G.; D'Aniel
Biochim. Biophys. Acta 1207, 217-222, 1994
A;Title: Properties of the flavoenzyme D-aspartate oxidase from Octopus vulgaris.
A;Reference number: S47624; MUID:94355383; PMID:7915543
A;Accession: S47624
A;Molecule type: protein
A;Residues: 1-28 <TED>
A;Cross-references: UNIPARC:UPI000017502F
A;Experimental source: hepatopancreas
C;Function:

A;Description: this enzyme is a flavoprotein that catalyzes the oxidative deamination of
A;Superfamily: D-amino-acid oxidase
C;Keywords: oxidoreductase; monomer; blocked amino end; FAD

```

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 5.9e+04;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAALKQKIASL 12
   ||| : :
Db 2 KIAIVAGVVGL 13

RESULT 24
JX0059
serine proteinase inhibitor MCEI-I - balsam pear
C;Species: Momordica charantia (Balsam pear, bitter melon)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JX0059
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0059
A;Molecule type: protein
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPROT:P10296; UNIPARC:UPI000012D226
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status predicted

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 22 ENDALQ 28
   : : : :
Db 13 DSDCLAQ 19

RESULT 25
A38232
vasoactive intestinal peptide - North American opossum
N;Alternate names: VIP
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A38232
R;Eng, J.; Yu, J.; Rattan, S.; Yalow, R.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 1809-1811, 1992
A;Title: Isolation and amino acid sequences of opossum vasoactive intestinal polypeptide
A;Reference number: A38232; MUID:92179271; PMID:1542675
A;Accession: A38232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <ENG>
A;Cross-references: UNIPROT:P39089; UNIPARC:UPI0000138846
A;Note: sequence extracted from NCBI backbone (NCBIP:87215)
C;Superfamily: glucagon
C;Keywords: duplication, intestine; neuropeptide

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 26.7%; Pred. No. 5.9e+04;
Matches 4; Conservative 7; Mismatches 2; Indels 2; Gaps 1;

QY 5 LKQKIASLKQEIADL 19
   ||| : : : :
Db 14 LKQ--MAMRKYLDSI 26

RESULT 26
S72460
ribosomal protein S19 - curled-leaved tobacco chloroplast (fragment)
C;Species: chloroplast Nicotiana glauca (curled-leaved tobacco)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S72460
R;Goulding, S.E.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
Mol. Gen. Genet. 252, 195-206, 1996

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A;Title: Ebb and flow of the chloroplast inverted repeat.
A;Reference number: S72459; MUID:96397499; PMID:8804393
A;Accession: S72460
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <GOU>
A;Cross-references: UNIPROT:Q36593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:g1279593; PII
A;Note: only a part of the nucleic acid sequence is shown
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
C;Genetics:
A;Gene: rps19
A;Genome: chloroplast
A;Start codon: GTG
C;Function:
A;Pathway: protein biosynthesis
C;Superfamily: ribosomal protein S19/S15
C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LKQEIADL 19
   : : : :
Db 15 LKKIDKL 22

RESULT 27
A23691
apolipoprotein C-I - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C;Accession: A23691
R;Weisgraber, K.H.; Mahley, R.W.; Kowal, R.C.; Herz, J.; Goldstein, J.L.; Brown, M.S.
J. Biol. Chem. 265, 22453-22459, 1990
A;Title: Apolipoprotein C-I modulates the interaction of apolipoprotein E with beta-migrator
ceptor-related protein.
A;Reference number: A23691; MUID:91093092; PMID:2266137
A;Accession: A23691
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <WEI>
A;Cross-references: UNIPROT:P33047; UNIPARC:UPI0000125C1C
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 28.6%; Pred. No. 5.9e+04;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 15 BIDALEYENDALEQ 28
   : : : : :
Db 3 DFSTLELIPDKLE 16

RESULT 28
S56746
alpha-synuclein, NAC - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S56746
R;Jensen, P.H.; Sorensen, E.S.; Petersen, T.E.; Gliemann, J.; Rasmussen, L.K.
Biochem. J. 310, 91-94, 1995
A;Title: Residues in the synuclein consensus motif of the alpha-synuclein fragment, NAC,
A;Reference number: S56746; MUID:95374478; PMID:7646476
A;Accession: S56746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <JEN>
A;Cross-references: UNIPARC:UPI0000179D22

Query Match      12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;

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Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IAALKQK 8
: : :
Db 15 VTAVAQK 21

RESULT 29

rRNA N-glycosidase (EC 3.2.2.22) saporin R1 - common soapwort (fragment)
C:Species: Saponaria officinalis (common soapwort)
C:Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S38524
R:Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Roc
Biochim. Biophys. Acta 1216, 31-42, 1993
A:Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA
A:Reference number: S38521; MUID:94032486; PMID:8218413
A:Accession: S38524
A:Molecule type: Protein
A:Residues: 1-28 <PER>
A:Cross-references: UNIPROT:Q7MI18; UNIPARC:UPI000017AF39
C:Keywords: glycosidase; hydrolase

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 19 LEYENDA 25
: : :
Db 8 LEFGQDS 14

RESULT 30

PC4430
peroxisome proliferator activated receptor gamma variant, P12A - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: PC4430
R:Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A:Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A:Reference number: PC4429; MUID:98086341; PMID:9425261
A:Accession: PC4430
A:Molecule type: DNA
A:Residues: 1-28 <YEN>
A:Cross-references: UNIPARC:UPI000017A1D0
C:Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C:Genetics:
A:Introns: 28/1

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 ASLKQK 15
: : :
Db 23 ANISQK 28

RESULT 31

PC4429
peroxisome proliferator activated receptor gamma - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: PC4429
R:Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A:Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A:Reference number: PC4429; MUID:98086341; PMID:9425261
A:Accession: PC4429
A:Molecule type: DNA
A:Residues: 1-28 <YEN>
A:Cross-references: UNIPARC:UPI000017A1CF

C:Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C:Genetics:
A:Introns: 28/1

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.9e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 ASLKQK 15
: : :
Db 23 ANISQK 28

RESULT 32

A31859
deoxycytidine kinase (EC 2.7.1.74) / deoxyadenosine kinase (EC 2.7.1.76) - Lactobacillus
C:Species: Lactobacillus acidophilus
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C:Accession: A31859
R:Ikeda, S.; Swenson, R.P.; Ives, D.H.
Biochemistry 27, 8648-8652, 1988
A:Title: Amino-terminal nucleotide-binding sequences of a Lactobacillus deoxynucleoside
A:Reference number: A31859; MUID:89118283; PMID:2851331
A:Accession: A31859
A:Molecule type: protein
A:Residues: 1-28 <IKE>
A:Cross-references: UNIPROT:Q7M0X4; UNIPARC:UPI0000175695
A:Note: 18-Ile, 21-Lys, 26-Gln, and 27-Ala were also found
C:Keywords: phosphotransferase

Query Match 12.9%; Score 17; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 5.9e+04;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 IAALKQKIASLKQK 15
: : :
Db 8 IGAGKSSLTGLLAE 21

RESULT 33

T47196
RAS protein [imported] - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47196
R:Lee, C.W.; Lee, E.
submitted to the EMBL Data Library, August 1995
A:Description: Structural analysis of ras genes from filamentous fungi.
A:Reference number: Z24384
A:Accession: T47196
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <LEE>
A:Cross-references: UNIPROT:P22126; UNIPARC:UPI000016891F; EMBL:U33746; PIDN:AAA74986.1
C:Genetics:
A:Gene: ras
A:Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 21.4%; Pred. No. 7.6e+04;
Matches 3; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 7 QKIASLKQKSIDALE 20
: : :
Db 4 RKQCTIDNEVALLD 17

RESULT 34

PH0231
T-cell receptor Vb CDR3, carrier PBL Vb 6.sbt - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 30-May-1997

C;Accession: PH0231
R;Hara, H.; Morita, M.; Iwaki, T.; Hatae, T.; Itoyama, Y.; Kitamoto, T.; Akizuki, S.; Goto, T.; submitted to JIPID, June 1994
A;Description: Detection of HTLV-I proviral DNA and analysis of T cell receptor Vb CDR3
A;Reference number: PH0227
A;Accession: PH0231
A;Molecule type: mRNA
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPARC:UPI000011C22C
A;Experimental source: spinal cord
C;Genetics:
A;Map position: 7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: receptor

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 80.0%; Pred. No. 7.6e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 ASLKQ 14
Db 3 ASSKQ 7

RESULT 35
D49829
T-cell receptor variable region beta chain, TCR Vbeta - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: D49829
R;Devaux, B.; Bjorkman, P.J.; Stevenson, C.; Greif, W.; Elliott, J.F.; Sagerstrom, C.; O'Garra, M.; Eur. J. Immunol. 21, 2111-2119, 1991
A;Title: Generation of monoclonal antibodies against soluble human T cell receptor polypeptide
A;Reference number: A49829; MUID:91364782; PMID:1832385
A;Accession: D49829
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-28 <DEV>
A;Cross-references: UNIPARC:UPI0000113F17; GB:S60796; NID:G235089; PIDN:AAB19725.1; PID:113
A;Experimental source: T-cell clone AL8.11
A;Note: sequence extracted from NCBI backbone (NCBIN:60796, NCBI:P:60804)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 75.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 LEYE 22
Db 9 LSYE 12

RESULT 36
S37683
protein IEF SSP 9124 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 09-Dec-1993 #sequence_revision 17-Nov-1995 #text_change 17-Nov-1995
C;Accession: S37683
R;Jeffers, H.; Madsen, P.; Rasmussen, H.H.; Honore, B.; Andersen, A.H.; Walbum, E.; Vanden Berghe, J. Mol. Biol. 231, 982-998, 1993
A;Title: Molecular cloning and expression of the transformation sensitive epithelial marker gene
A;Reference number: S34753; MUID:93294871; PMID:8515476
A;Accession: S37683
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <LEF>
A;Cross-references: UNIPARC:UPI000017C320

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 27.3%; Pred. No. 7.6e+04;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 13 KOEIDALEYEN 23
Db 1 EQLVNVTELN 11

RESULT 37
PS0106
2-phosphinomethylmalic acid synthase - Streptomyces hygroscopicus (fragment)
N;Alternate names: PMM synthase
C;Species: Streptomyces hygroscopicus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: PS0106
R;Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H. Agric. Biol. Chem. 54, 463-470, 1990
A;Title: Purification and characterization of citrate synthase from Streptomyces hygroscopicus
A;Reference number: PS0106; MUID:90334852; PMID:1368511
A;Accession: PS0106
A;Molecule type: DNA
A;Residues: 1-28 <SHI>
A;Cross-references: UNIPROT:Q9LCB4; UNIPROT:Q03618; UNIPARC:UPI000017AE21
A;Experimental source: strain SF-1293
C;Comment: This enzyme catalyzes the condensation reaction between phosphinopyruvic acid and pyruvate

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 YENDALEQ 28
Db 16 FPQDAFPQ 23

RESULT 38
A69259
hypothetical protein AF0073 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69259
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Ariach, P.; Kaine, B.P.; Sykes, S.N.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeobacterium Pyrococcus furiosus
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69259
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <KLE>
A;Cross-references: UNIPROT:Q30163; UNIPARC:UPI0000057244; GB:AE001101; GB:AE000782; NID:113

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KOEID 17
Db 16 RAEID 20

RESULT 39
T09594
gene LFY protein - Monterey pine (fragment)
C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09594
R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R. submitted to the EMBL Data Library, August 1996
A;Description: Partial characterization of Pinus radiata meristem identity homolog gene
A;Reference number: Z16756
A;Accession: T09594
A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-28 <I20>
A:Cross-references: UNIPROT:O24285; UNIPARC:UPI000000AC80; EMBL:U66725; NID:gl513305; PID:
C:Genetics:
A:Gene: LFY
C:Function:
A:Description: controls meristem identity

Query Match 12.1%; Score 16; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ALKQK 8
||:|
Db 14 ALRKK 18

RESULT 40

I68614
frame shifted FMR1 exon - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
A:Accession: I68614; I68615
R:Richier, E.E.; Richards, S.; Gibbs, R.A.; Nelson, D.L.
Hum. Mol. Genet. 2, 1147-1153, 1993
A:Title: Fine structure of the human FMR1 gene.
A:Reference number: I54334; MUID:94004853; PMID:8401496
A:Accession: I68614
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <E11>
A:Cross-references: UNIPROT:Q16578; UNIPARC:UPI0000006DB1C; GB:L19490; NID:g388747; PIDN:
A:Accession: I68615
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <E12>
A:Cross-references: UNIPARC:UPI0000006DB1C; GB:L19491; NID:g388749; PIDN:AAA62467.1; PID:
C:Comment: This sequence appears to be the frame shifted hypothetical translation of an
C:Genetics:
A:Gene: GDB:FMR1
A:Cross-references: GDB:I29038; OMIM:309550
A:Map position: Xq27.3-Xq27.3

Query Match 12.1%; Score 16; DB 4; Length 28;
Best Local Similarity 75.0%; Pred. No. 7.6e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LKQE 15
||:|
Db 18 LKEE 21

RESULT 41

T14210
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastix acanthinurus mitochond
C:Species: Mitochondrion Uromastix acanthinurus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A:Accession: T14210
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826; PMID:9000757
A:Accession: T14210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <MAC>

A:Cross-references: UNIPROT:P92760; UNIPARC:UPI0000099123; EMBL:U71325; NID:gl753264; PI
A:Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, Univers
C:Genetics:
A:Gene: ND1
A:Note: ND1
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 30.8%; Pred. No. 9.6e+04;
Matches 4; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 11 SLKQEIDALEYEN 23
||:|
Db 15 NLPALALPPDN 27

RESULT 42

T12301
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Dipsosaurus dorsalis mitochondri
C:Species: Mitochondrion Dipsosaurus dorsalis
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
A:Accession: T12301
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usin
A:Reference number: Z17488; MUID:99162288; PMID:10051389
A:Accession: T12301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <SCH>
A:Cross-references: UNIPROT:Q9ZYV5; UNIPARC:UPI000008FBBF; EMBL:AF049857; NID:g4105726;
A:Experimental source: specimen voucher Museum of Vertebrate Zoology, Berkeley, Californ
C:Genetics:
A:Genome: mitochondrion
A:Note: ND1
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 9.6e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 SLKQEIDAL 19
||:|
Db 15 SLPTSIFAL 23

RESULT 43

A60291
24K proteinase (EC 3.4.-.-) - silkworm (fragment)
C:Species: Bombyx mori (silkworm)
C:Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 15-Oct-1999
A:Accession: A60291
R:Ikedo, M.; Sasaki, T.; Yamashita, O.
Insect Biochem. 20, 725-734, 1990
A:Title: Purification and characterization of proteases responsible for vitellin degrada
A:Reference number: A60291
A:Accession: A60291
A:Molecule type: protein
A:Residues: 1-28 <IKE>
A:Cross-references: UNIPARC:UPI0000175C3C
C:Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenes
C:Superfamily: trypsin; trypsin homology
C:Keywords: egg yolk; hydrolase

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 9.6e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AALKQKIASL 12
||:|
Db 19 ASMXNXIAL 28

RESULT 44

S55729
orotidine-5'-monophosphate decarboxylase - Aspergillus awamori (fragments)
C:Species: Aspergillus awamori
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004

C;Accession: S55729
R;Gouka, R.J.; Heesing, J.G.M.; Stam, H.; Musters, W.; van den Hondel, C.A.M.J.J.
Curr. Genet. 27, 536-540, 1995
A;Title: A novel strategy for the isolation of defined pyrG mutants and the development
A;Reference number: S55729; MUID:96031709; PMID:7553938
A;Accession: S55729
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18;19-28 <GOU>
A;Cross-references: UNIPARC:UPI0000069725; UNIPARC:UPI0000175F90
C;Superfamily: Orotidine-5'-phosphate decarboxylase; orotidine-5'-phosphate decarboxylase

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 22.2%; Pred. No. 9.6e+04;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 IASLKOEID 17

Db 7 VTTKELLD 15

RESULT 45

JX0058
trypsin inhibitor MCTI-II - balsam pear
C;Species: Momordica charantia (balsam pear, bitter melon)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JX0058
R;Hara, S.; Makino, J.; Ikenaka, T.
J. Biochem. 105, 88-92, 1989
A;Title: Amino acid sequences and disulfide bridges of serine proteinase inhibitors from
A;Reference number: JX0057; MUID:89291812; PMID:2738047
A;Accession: JX0058
A;Molecule type: protein
A;Residues: 1-28 <HAR>
A;Cross-references: UNIPROT:P10295; UNIPARC:UPI000012DA53
C;Superfamily: squash trypsin inhibitor ITD I
C;Keywords: serine proteinase inhibitor
F;3-20,10-22,16-27/Disulfide bonds: #status experimental

Query Match 11.4%; Score 15; DB 2; Length 28;
Best Local Similarity 28.6%; Pred. No. 9.6e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 22 ENDALEQ 28

Db 13 DSDCMAQ 19

Search completed: November 21, 2005, 21:47:32
Job time : 25.5 secs


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RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcription, and proteomic analyses.";
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; CAA01003874; CA01121.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3516 MW; 1A2DFD1935C265AE CRC64;

Query Match 23.5%; Score 31; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.2e+04;
Matches 5; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 KOKIASLKQEI DALEYEND 24
Db 2 KQKLLKIEMRKDGCGRYHE 20

RESULT 3
O65311 ARATH
ID O65311 ARATH PRELIMINARY; PRT; 28 AA.
AC O65311;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-9 tubulin (Fragment).
GN Name=TUB9;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sanders P.M., Bui A.Q., Weterings K., McIntire K.N., Hau Y.C.,
RA Lee P.Y., Truong M.T., Beals T.B., Goldberg R.B.;
RT "Another Development Defects in Arabidopsis thaliana Male-Sterile
RT Mutants.";
RL Sex. Plant Reprod. 11:297-322(1999).
DR EMBL; AF060248; AAC97107.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 28 AA; 3388 MW; 8060E4E537BE670E CRC64;

Query Match 22.7%; Score 30; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.5e+04;
Matches 9; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

QY 9 IASLKQEI DAL----EYENDALEQ 28
Db 3 VAEEVQVQDATVGEVEEVEDEEE 26

RESULT 4
Q9RAT7 LACLC
ID Q9RAT7 LACLC PRELIMINARY; PRT; 28 AA.
AC Q9RAT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA ligase homolog (Fragment).
GN Name=lig;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Petersen A., Josephsen J., Johnsen M.G.;
RX MEDLINE=20026817; PubMed=10559170;
RA "fW22, a lactococcal temperate phage with a site-specific integrate

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RT closely related to Streptococcus thermophilus phage integrases.";
RL J. Bacteriol. 181:7034-7042(1999).
DR EMBL; AF065985; AAF13028.1; -; Genomic DNA.
DR GO; GO:0003911; F:DNA ligase (NAD+) activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR001679; DNAligase.
DR Pfam; PF01653; DNA_ligase_aden; 1.
KW Ligase.
FT NON TER 28
SQ SEQUENCE 28 AA; 3418 MW; 532F398A7706A580 CRC64;

Query Match 21.2%; Score 28; DB 2; Length 28;
Best Local Similarity 20.8%; Pred. No. 2.7e+04;
Matches 5; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 5 LKQIASLKQEI DALEYENDALEQ 28
Db 3 IESKKEFTDQLNQFAEYITLDE 26

RESULT 5
O4TIF5 TETNG
ID O4TIF5 TETNG PRELIMINARY; PRT; 28 AA.
AC O4TIF5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2190, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00038313001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutacheau J.P., Guzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01002190; CAF87327.1; -; Genomic_DNA.
FT NON TER 28
SQ SEQUENCE 28 AA; 3040 MW; 776D95631570A999 CRC64;

Query Match 19.7%; Score 26; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 4.7e+04;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 AALKQKIASLKQEI 16
Db 11 AEVRAKLAELELEL 24

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RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL NATURE 420:316-320(2002).
DR EMBL; AL62998; CAD41522.2; -; Genomic_DNA.
DR Gramene; Q7XU72; -.
SQ SEQUENCE 28 AA; 3150 MW; 715B4E08C513DCD3 CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 6.1e+04;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 ASLKQEIIDALEYEN 23
DB 13 ASLRMELEGKIFWN 26

RESULT 8
Q9XGE4 VICFA
ID Q9XGE4 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonuclease H (Fragment).
GN Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OC NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243103; CAB45147.1; -; Genomic_DNA.
DR InterPro; IPR000886; ER_target_S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 28 AA; 3187 MW; 1213C2C39C722B7C CRC64;

Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.1e+04;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 IDALEYEN 23
DB 8 LDANQFEN 15

RESULT 9
Q80KE6 9RHAB
ID Q80KE6 9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KE6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OC NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paez A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192396; AAO45871.1; -; Genomic_RNA.
FT NON_TER 28

us-10-088-417a-1.rup

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SQ SEQUENCE 28 AA; 3068 MW; 2F7337A9AAC95C6A CRC64;
Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. NO. 6.1e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 16 IDALEYENDALE 27
|| : || || |
DB 12 IDPIESEADPRE 23

RESULT 10
Q6DQ01_9RHAB
ID Q6DQ01_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q6DQ01;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Polymerase (Fragment).
GN Names;
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C52/98;
RA Paez A., Saad C., Nunez C., Boshell J.;
RT "Molecular epidemiology of rabies in northern Colombia 1994-2003: evidence for human and fox rabies associated with dogs.";
RL Epidemiol. Infect. 133:529-536(2005).
DR EMBL; AV649921; AAT66971.1; -; Genomic_RNA.
FT NON TER 28
SQ SEQUENCE 28 AA; 3068 MW; 2F7337A9AAC95C6A CRC64;
Query Match 18.9%; Score 25; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. NO. 6.1e+04;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 16 IDALEYENDALE 27
|| : || || |
DB 12 IDPIESEADPRE 23

RESULT 11
Q38269_LAMB
ID Q38269_LAMB PRELIMINARY; PRT; 28 AA.
AC Q38269;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf28.
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC DOI=10.1146/annurev.bi.47.070178.004535;
RA Adhya S., Gottesman M.;
RT "Control of transcription termination.";
RL Annu. Rev. Biochem. 47:967-996(1978).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=83189071; PubMed=6221115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT "Nucleotide sequence of bacteriophage lambda DNA.";
RL J. Mol. Biol. 162:729-773(1982).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=73215915; PubMed=4515613;
RA Weigel P.H., Englund P.T., Murray K., Old R.W.;
RT "The 3'-terminal nucleotide sequences of bacteriophage lambda DNA.";
Proc. Natl. Acad. Sci. U.S.A. 70:1151-1155(1973).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=82059489; PubMed=6458018;
RA Ieichen K., Shepherd J.C.W., Bickle T.A.;
RT "The DNA sequence of the phage lambda genome between PL and the gene bet.";
RL Nucleic Acids Res. 9:4639-4653(1981).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=84170247; PubMed=6324174;
RA Hohn B.;
RT "DNA sequences necessary for packaging of bacteriophage lambda DNA.";
Proc. Natl. Acad. Sci. U.S.A. 80:7456-7460(1983).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85074479; PubMed=6096022; DOI=10.1016/0092-8674(84)90478-1;
RA Craig N.L., Nash H.A.;
RT "E. coli integration host factor binds to specific sites in DNA.";
Cell 39:707-716(1984).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85083055; PubMed=6096550;
RA Edling T.D., Cooley T.E., Richards S.H., Ihler G.M.;
RT "Long range base-pairing in the leftward transcription unit of bacteriophage lambda. Characterization by electron microscopy and computer-aided sequence analysis.";
J. Mol. Biol. 179:351-365(1984).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85083885; PubMed=6096564;
RA Frackman S., Siegele D.A., Feiss M.;
RT "A functional domain of bacteriophage lambda terminase for prohead binding.";
J. Mol. Biol. 180:283-300(1984).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85134899; PubMed=6241264;
RA Place N., Fien K., Mahoney M.E., Wulff D.L., Ho Y.S., Debouck C., Rosenberg M., Shih M.C., Gussin G.N.;
RT "Mutations that alter the DNA binding site for the bacteriophage lambda cII protein and affect the translation efficiency of the cII gene.";
J. Mol. Biol. 180:865-880(1984).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=84119525; PubMed=6229793;
RA Wulff D.L., Mahoney M., Shatzman A., Rosenberg M.;
RT "Mutational analysis of a regulatory region in bacteriophage lambda that has overlapping signals for the initiation of transcription and translation.";
Proc. Natl. Acad. Sci. U.S.A. 81:555-559(1984).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=84222010; PubMed=6233610;
RA Warren F., Das A.;
RT "Formation of termination-resistant transcription complex at phage lambda nut locus: effects of altered translation and a ribosomal mutation.";
Proc. Natl. Acad. Sci. U.S.A. 81:3612-3616(1984).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85232076; PubMed=2408965; DOI=10.1016/0378-1119(85)90139-8;
RA Coleclough C., Erlitz F.L.;
RT "Use of primer-restriction-end adapters in a novel cDNA cloning strategy.";
Gene 34:305-314(1985).
RN [13]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85142185; PubMed=3156406;
RA Peltz S.W., Brown A.L., Hasan N., Podhajek A.J., Szybalski W.;
RT "Thermosensitivity of a DNA recognition site: activity of a truncated
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RT  ntL antiterminator of coliphage lambda.";
RL  Science 228:91-93(1985).
RN  [14]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=87280224; PubMed=3038914;
RA  Chen C.Y., Richardson J.P.;
RT  "Sequence elements essential for rho-dependent transcription
RL  termination at lambda trl.";
RJ  J. Biol. Chem. 262:11292-11299(1987).
RN  [15]
RP  NUCLEOTIDE SEQUENCE.
RA  Daniels D.L., Schroeder J.L., Szybalski W., Sanger F., Coulson A.R.,
RA  Hong G.F., Hill D.F., Petersen G.B., Blattner F.R.;
RT  "Appendix II: Complete annotated lambda sequence.";
RL  (in) Hendrix R.W., Roberts J.W., Stahl F.W., Weisberg R.A. (eds.);
RL  LAMBDA II, pp.519-674, Cold Spring Harbor Laboratory, Cold Spring
RL  Harbor (1983).
RN  [16]
RP  NUCLEOTIDE SEQUENCE.
RA  Daniels D.L., Schroeder J.L., Szybalski W., Sanger F., Blattner F.R.;
RT  "Appendix I: A molecular map of coliphage lambda.";
RL  (in) Hendrix R.W., Roberts J.W., Stahl F.W., Weisberg R.A. (eds.);
RL  LAMBDA II, pp.469-517, Cold Spring Harbor Laboratory, Cold Spring
RL  Harbor (1983).
DR  EMBL: J02459; AAA96576.1; -; Genomic DNA.
SQ  SEQUENCE 28 AA; 3699 MW; 2011F5C89C669BE2 CRC64;

Query Match 18.6%; Score 24.5; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 7e+04;
Matches 5; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 12 LKQETDAL-EYENDALEQ 28
Db 1 MESEFEFEHPQDVMEQ 18

RESULT 12
QSPF48_SALPA
ID QSPF48_SALPA PRELIMINARY; PRT; 28 AA.
AC QSPF48;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=SPA2417;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE.
STRAIN=ATCC 9150;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton C., Nash W., Miner T., Minx P.,
RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3699 MW; 2011F5C89C669BE2 CRC64;

Query Match 18.6%; Score 24.5; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 7e+04;
Matches 5; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Qy 12 LKQETDAL-EYENDALEQ 28
Db 1 MESEFEFEHPQDVMEQ 18

RESULT 13
Q9URD3_ASPOR
ID Q9URD3_ASPOR PRELIMINARY; PRT; 28 AA.
AC Q9URD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Phosphatidylglycerol/phosphatidylinositol transfer protein (Fragment).
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95260846; PubMed=7742351; DOI=10.1016/0005-2760(94)00252-T;
RA Record E., Asther M., Marion D., Asther M.;
RT "Purification and characterization of a novel specific
RT phosphatidylglycerol-phosphatidylinositol transfer protein with high
RT activity from Aspergillus oryzae.";
RL Biochim. Biophys. Acta 1256:18-24(1995).
SQ SEQUENCE 28 AA; 3015 MW; 95BB1828F1855D14 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 83.3%; Pred. No. 8.1e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 LEYEND 24
Db 10 LEYCND 15

RESULT 14
Q6B3M0_9DIPT
ID Q6B3M0_9DIPT PRELIMINARY; PRT; 28 AA.
AC Q6B3M0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE 6-phosphogluconate dehydrogenase (Fragment).
GN Name=pgd;
OS Drosophila polymorpha.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=133991;
RN [1]
RP NUCLEOTIDE SEQUENCE.
STRAIN=116_9M.2, 119_8F.1, CC8M, CC8F, CC8M.3, CF 4M, CF 5M, CF 9M,
RC D8.1, D8.2, D8.3, Fe-8F.2, TUN 7F, TUN 7F.1, LAG8F.2, Furn 7,
RC Sertao_6M.1, Sertao_7M, Sr_9MP, UFRGS 7M.1, UFRGS 8M.3, USPR_9M.1,
RC U28.6, AB.5, AB.5, B8.5, B8.5, C8.7, 116_8M.1, and 116_8M.3;
RA Brissot J.A., Templeton A.R., Duncan I.;
RT "Population Genetics of the Developmental Gene optomotor-blind (omb)
RT in Drosophila polymorpha. Evidence for a Role in Abdominal
RT Pigmentation Variation.";
RL Genetics 168:1999-2010(2004).
DR EMBL: AY687197; AAT90600.1; -; Genomic DNA.
DR EMBL: AY687202; AAT90605.1; -; Genomic DNA.
DR EMBL: AY687206; AAT90609.1; -; Genomic DNA.
DR EMBL: AY687210; AAT90613.1; -; Genomic DNA.
DR EMBL: AY687217; AAT90620.1; -; Genomic DNA.
DR EMBL: AY687219; AAT90622.1; -; Genomic DNA.
DR EMBL: AY687227; AAT90630.1; -; Genomic DNA.
DR EMBL: AY687231; AAT90634.1; -; Genomic DNA.
DR EMBL: AY687234; AAT90637.1; -; Genomic DNA.
DR EMBL: AY687268; AAT90671.1; -; Genomic DNA.
DR EMBL: AY687286; AAT90669.1; -; Genomic DNA.
DR EMBL: AY687264; AAT90667.1; -; Genomic DNA.
DR EMBL: AY687261; AAT90664.1; -; Genomic DNA.
DR EMBL: AY687255; AAT90658.1; -; Genomic DNA.

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DR EMBL; AY687253; AAT90656.1; -; Genomic DNA.
DR EMBL; AY687251; AAT90654.1; -; Genomic DNA.
DR EMBL; AY687250; AAT90653.1; -; Genomic DNA.
DR EMBL; AY687246; AAT90649.1; -; Genomic DNA.
DR EMBL; AY687193; AAT90596.1; -; Genomic DNA.
DR EMBL; AY687279; AAT90682.1; -; Genomic DNA.
DR EMBL; AY687278; AAT90681.1; -; Genomic DNA.
DR EMBL; AY687273; AAT90676.1; -; Genomic DNA.
DR EMBL; AY687271; AAT90674.1; -; Genomic DNA.
DR EMBL; AY687233; AAT90636.1; -; Genomic DNA.
DR EMBL; AY687229; AAT90632.1; -; Genomic DNA.
DR EMBL; AY687226; AAT90629.1; -; Genomic DNA.
DR EMBL; AY687218; AAT90621.1; -; Genomic DNA.
DR EMBL; AY687211; AAT90614.1; -; Genomic DNA.
DR EMBL; AY687207; AAT90610.1; -; Genomic DNA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004616; F:phosphoglucanate dehydrogenase (decarboxyla. .; IEA.
DR GO; GO:0006098; P:pentose-phosphate shunt; IEA.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3130 MW; 79BEB7C173784FC CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.1e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 SLKQEIDALEY 20
   ||| :| :|
Db 7 SLKDMVDKLG 16

RESULT 15
Q9TXX0 MANSE
ID Q9TXX0 MANSE PRELIMINARY; PRT; 28 AA.
AC Q9TXX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cell surface protein 295 91 kDa component (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92331807; PubMed=1628754;
RA Nardi J.B.;
RT "Dynamic expression of a cell surface protein during rearrangement of
RT epithelial cells in the Manduca wing monolayer."
RL Dev. Biol. 152:161-171(1992).
DR PIR; A44877; A44877.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3271 MW; 28D250E730958651 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.1e+04;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 12 LKQEIDALEYEN 23
   :|::|::|
Db 14 VKQIESFEVIN 25

RESULT 16
Q4XF30 PLACH
ID Q4XF30 PLACH PRELIMINARY; PRT; 28 AA.
AC Q4XF30;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).

GN ORENames=PC402326.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01006830; CAH84488.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3456 MW; A553FF68D5BA9A08 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 8.1e+04;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LKQKTASLK 13
   :|::| :|
Db 12 LRKKINTLK 20

RESULT 17
Q4YIJ2 PLABE
ID Q4YIJ2 PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YIJ2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB400921.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAI01003873; CAI01119.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3293 MW; EB2333D901B77433 CRC64;

Query Match 18.2%; Score 24; DB 2; Length 28;
Best Local Similarity 30.8%; Pred. No. 8.1e+04;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 9 IASLKQEIDALEY 21
   :|::| :|
Db 1 LBSLKKRVSQLSF 13

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RESULT 18
Q4X244_ASPFU PRELIMINARY; PRT; 28 AA.
ID Q4X244
AC Q4X244
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Afu2g07740;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Niernman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman N., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kunagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouny I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penvalva M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinovitch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000001; EAL93071.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3148 MW; EED31A7594D35F59 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 26.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 9 IASLKQEDALEYEN 23
Db 3 ILLKSQITLDFDS 17

RESULT 19
Q4XER1_PLACH PRELIMINARY; PRT; 28 AA.
ID Q4XER1
AC Q4XER1
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC402453.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; CAAJ01006927; CAH84607.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3187 MW; 8A41A233470265ED CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 16 IDALEYEND 24
Db 10 ISALRVGND 18

RESULT 20
Q4YA09_PLABE PRELIMINARY; PRT; 28 AA.
ID Q4YA09
AC Q4YA09
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PBI01343.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL; CAAI01007241; CAI05471.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3629 MW; OCDB27595925A4B0 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIAALKKQIASLKQ 15
Db 5 QIKQKKQKTQKMKK 19

RESULT 21
O62731_CANFA PRELIMINARY; PRT; 48 AA.
ID O62731
AC O62731
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tropomyosin (Fragment).
GN Name=TPM1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.

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OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049587; AAC05499.1; -; Genomic DNA.
DR Ensembl; ENSCARG00000016966; Canis familiaris.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 KQIASLKQEI 16
Db 12 ESKCAELEEL 22

RESULT 22
Q80KK2_9RHAB
ID Q80KK2_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KK2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192412; AAO31967.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2996 MW; 2F7337A9AAC3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
Db 12 IDPISEAD 20

RESULT 23
Q80KLI_9RHAB
ID Q80KLI_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KLI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192403; AAO31958.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2938 MW; 2F7335C43ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
Db 12 IDPISEAD 20

RESULT 24
Q80KLI_9RHAB
ID Q80KLI_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q80KLI;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE L protein (fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA Paz A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AY192400; AAO31955.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2966 MW; 2F7335C425DA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
Db 12 IDPISEAD 20

RESULT 25
Q6DQP6_9RHAB
ID Q6DQP6_9RHAB PRELIMINARY; PRT; 28 AA.
AC Q6DQP6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Polymerase (fragment).
GN Name=L;
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
OX NCBI_TaxID=11292;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C44/97;
RA Paz A., Saad C., Nunez C., Boshell J.;
RT "Molecular epidemiology of rabies in northern Colombia 1994-2003:
evidence for human and fox rabies associated with dogs.";
RL Epidemiol. Infect. 133:529-536(2005).
DR EMBL; AY649926; AAT66976.1; -; Genomic_RNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 2938 MW; 2F7335C43ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 1.1e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 16 IDALEYEND 24
 ||:|:|
 Db 12 IDPIESEAD 20

RESULT 26

Q6DQ03_9RHAB PRELIMINARY; PRT; 28 AA.
 AC Q6DQ03_9RHAB PRELIMINARY; PRT; 28 AA.
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Polymerase (Fragment).
 GN Name=L; virus.
 OS Rabies virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OX NCBI_TaxID=11292;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C41/97;
 RA Paez A., Saad C., Nunez C., Boshell J.;
 RT "Molecular epidemiology of rabies in northern Colombia 1994-2003:
 RT evidence for human and fox rabies associated with dogs.";
 RL Epidemiol. Infect. 133:529-536(2005).
 DR EMBL; AY649919; AAT66969.1; -; Genomic_RNA.
 FT NON TER 28
 SQ SEQUENCE 28 AA; 2996 MW; 2F7337A9ACA3C6A CRC64;

Query Match 17.4%; Score 23; DB 2; Length 28;
 Best Local Similarity 55.6%; Pred. No. 1.1e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 IDALEYEND 24
 ||:|:|
 Db 12 IDPIESEAD 20

RESULT 27

Q9NCS6 TRYCR PRELIMINARY; PRT; 28 AA.
 AC Q9NCS6 TRYCR PRELIMINARY; PRT; 28 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Tcpl7 protein (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 OX NCBI_TaxID=5693;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SO3;
 EX MEDLINE=20231759; PubMed=10767555; DOI=10.1016/S0378-1119(00)00074-3;
 RA Robello C., Gamarro F., Castanys S., Alvarez-Valin F.;
 RT "Evolutionary relationships in Trypanosoma cruzi: molecular
 RT phylogenetics supports the existence of a new major lineage of
 RT strains.";
 RL Gene 246:331-338(2000).
 DR EMBL; AF174410; AAF97119.1; -; Genomic_DNA.
 DR InterPro; IPR006175; Endoribon_LPSF.
 DR Pfam; PF01042; Ribonuc L-PSF; 1.
 FT NON TER 1
 SQ SEQUENCE 28 AA; 2807 MW; 14910A845047712 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 80.0%; Pred. No. 1.4e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 BIDAL 19
 ||:|:|
 Db 19 EVDAL 23

RESULT 28

Q4X811 PLACH PRELIMINARY; PRT; 28 AA.
 AC Q4X811 PLACH PRELIMINARY; PRT; 28 AA.
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PC405179.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01009035; CAH86965.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 28 AA; 3537 MW; 9F44F6D16F101DA CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 8 KIASLKOEIDALEYH 22
 ||:|:|:|
 Db 3 KIRKIFAEENNEINYE 17

RESULT 29

Q4YAC7 PLABE PRELIMINARY; PRT; 28 AA.
 AC Q4YAC7 PLABE PRELIMINARY; PRT; 28 AA.
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB401815.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01007122; CAI05297.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 28 AA; 3288 MW; 52CB801BB1CD1F21 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
 Best Local Similarity 41.7%; Pred. No. 1.4e+05;

Best Local Similarity 21.1%; Pred. No. 1.4e+05; Mismatches 5; Indels 0; Gaps 0;	
QY	9 IASLKQEI DALEYENDAL 27
Db	4 VXXYXEAQVQVNYAXE 22
RESULT 34	
ID	Q5F210_MOUSE PRELIMINARY; PRT; 28 AA.
AC	Q5F210; 2005 (Tremblrel. 30, Created)
DT	10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT	10-MAY-2005 (Tremblrel. 30, Last sequence update)
DE	Oxytelor binding protein 2 (Fragment)
GN	Names=Osbp2; ORFNames=RP23-309E11.7-004;
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Dunn M.;
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL731853; CA151856.1; -; Genomic_DNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3453 MW; 2BF5DACD2D68FCFC CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 57.1%; Pred. No. 1.4e+05;	
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY	18 ALEYEND 24
Db	22 ALNYEQE 28
RESULT 35	
ID	Q80KF1_9RHAB PRELIMINARY; PRT; 28 AA.
AC	Q80KF1; 2003 (Tremblrel. 24, Created)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE	L protein (Fragment)
OS	Rabies virus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Lyssavirus.
OX	NCBI_TaxID=11292;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT	human and dog rabies associated with bats."
RL	J. Gen. Virol. 84:795-802(2003).
DR	EMBL; AY192391; AAO45866.1; -; Genomic_RNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3153 MW; 2E3266A9AAD64C6A CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 44.4%; Pred. No. 1.4e+05;	
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 IDALEYEND 24
Db	12 IDPIESEDE 20
RESULT 36	
ID	Q80KG5_9RHAB PRELIMINARY; PRT; 28 AA.
AC	Q80KG5; 2003 (Tremblrel. 24, Created)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT	01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE	L protein (Fragment)
OS	Rabies virus.
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC	Rhabdoviridae; Lyssavirus.
OX	NCBI_TaxID=11292;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	MEDLINE=22541850; PubMed=12655080; DOI=10.1099/vir.0.18899-0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT	human and dog rabies associated with bats."
RL	J. Gen. Virol. 84:795-802(2003).
DR	EMBL; AY192391; AAO45866.1; -; Genomic_RNA.
FT	NON_TER 28
SQ	SEQUENCE 28 AA; 3153 MW; 2E3266A9AAD64C6A CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 44.4%; Pred. No. 1.4e+05;	
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
QY	16 IDALEYEND 24
Db	12 IDPIESEDE 20
RESULT 37	
ID	Q9PRN8_CARAU PRELIMINARY; PRT; 28 AA.
AC	Q9PRN8; 2000 (Tremblrel. 13, Created)
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE	GVIP-VASOACTIVE intestinal peptide.
OS	Carassius auratus (Goldfish)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Carassius.
OX	NCBI_TaxID=7957;
RN	[1]
RP	PROTEIN SEQUENCE.
RA	MEDLINE=96051491; PubMed=8536941; DOI=10.1006/gcen.1995.1113;
RA	Uesaka T., Yano K., Yamasaki M., Ando M.;
RT	"Somatostatin-, vasoactive intestinal peptide-, and granulin-like
RT	peptides isolated from intestinal extracts of goldfish, Carassius
RT	auratus."
RL	Gen. Comp. Endocrinol. 99:298-306(1995).
DR	HSSP; P18509; IGEA.
DR	GO; GO:0005576; C:extracellular region; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
DR	InterPro; IPR000532; Glucagon.
DR	Pfam; PF00123; Hormone 2; 1.
DR	PRINTS; PR00275; GLUCAGON.
DR	SMART; SM00070; GLUCA; 1.
DR	PROSITE; PS00260; GLUCAGON; 1.
SQ	SEQUENCE 28 AA; 3278 MW; E706A67573FF6F2F CRC64;
Query Match 16.7%; Score 22; DB 2; Length 28;	
Best Local Similarity 20.8%; Pred. No. 1.4e+05;	
Matches 5; Conservative 6; Mismatches 13; Indels 0; Gaps 0;	
QY	3 AALKQKIATSLKQEI DALEYENDAL 26
Db	4 AVFTDYSRYEKQMAKKYLSVL 27
RESULT 38	
ID	Q4RLC7_TETNG PRELIMINARY; PRT; 28 AA.

RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."; RT
RN Nature 431:946-957(2004). [2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; CAAE01014601; CAG00546.1; -: Genomic DNA.
SQ SEQUENCE 28 AA; 3111 MW; FB98EC78D4C0EECE CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 35.7%; Pred. No. 1.4e+05;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 13 KBIDALEVENDAL 26
Db 8 EEIQFLRTVSdav 21
::||| | :|||

RESULT 40
QAT3NS_TETNG PRELIMINARY; PRT; 28 AA.

AC QAT3NS;
CD 13-SEP-2005 (TtEMBLrel. 31, Created)
DT 13-SEP-2005 (TtEMBLrel. 31, Last sequenced update)
DT 13-SEP-2005 (TtEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAP9978, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG0007715001;
GN Tetraodon nigroviridis (Green puffer).
OS Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RP Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castello L., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Bernardis V.,
RA Craud C., Duprat S., Brottier P., Coutancheau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004). [2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR ENBL; CAAE01009978; CAF92497.1; -: Genomic DNA.
FT NON TER 1
FT NON TER 28
SQ SEQUENCE 28 AA; 3037 MW; 996E33BD98146314 CRC64;

Query Match 16.7%; Score 22; DB 2; Length 28;
Best Local Similarity 31.2%; Pred. No. 1.4e+05;

Matches	5; Conservative	5; Mismatches	6; Indels	0; Gaps	0;
5 LKQKIASLKQETDALE 20					
3 LREAVALLTAQQTSL 18					
RESULT 41					
Q4XPA5	PLACH PRELIMINARY;	PRT;	28 AA.		
Q4XPA5;					
13-SEP-2005	(TrEMBLrel. 31, Created)				
13-SEP-2005	(TrEMBLrel. 31, Last sequence update)				
13-SEP-2005	(TrEMBLrel. 31, Last annotation update)				
Hypothetical protein.					
ORFNames=PC108138.00.0;					
Plasmodium chabaudi.					
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.					
NCBI_TaxID=5825;					
[1]					
NUCLEOTIDE SEQUENCE.					
Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,					
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,					
James K., Rutherford K., Harris B., Harris D., Churcher C.,					
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,					
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,					
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,					
"A comprehensive survey of the Plasmodium life cycle by genomic,					
transcriptomic, and proteomic analyses."					
Science 307:82-86 (2005).					
-!- CAUTION: The sequence shown here is derived from an					
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is					
preliminary data.					
EMBL; CAJ01004227; CAH81257.1; -; Genomic_DNA.					
Hypothetical protein.					
SEQUENCE 28 AA; 3205 MW; OE80FBB396A347AC CRC64;					
Query Match	16.3%;	Score 21.5;	DB 2;	Length 28;	
Best Local Similarity	42.9%;	Pred. No. 1.6e+05;			
Matches	6;	Conservative 4;	Mismatches 3;	Indels 1;	Gaps 1;
1 KIAALKQKIASLKQ 14					
15 KVLFIK-KLKSLLK 27					
SULT 42					
2_BRANA	STANDARD;	PRT;	28 AA.		
Q96353;					
01-NOV-1997	(Rel. 35, Created)				
01-NOV-1997	(Rel. 35, Last sequence update)				
10-MAY-2005	(Rel. 47, Last annotation update)				
Metallothionein-like protein type 2 LSC210 (Fragment).					
Name=LSC210;					
Brassica napus (Rape).					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;					
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.					
NCBI_TaxID=3708;					
[1]					
NUCLEOTIDE SEQUENCE.					
STRAIN=cv. Falcon; TISSUE=Leaf;					
Buchanan-Wollaston V., Ainsworth C.;					
Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.					
-!- FUNCTION: Metallothioneins have a high content of cysteine					
residues that bind various heavy metals.					
-!- SIMILARITY: Belongs to the metallothionein superfamily. Type 15					
family.					
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between the Swiss Institute of Bioinformatics and the EMBL outstation -					
the European Bioinformatics Institute. There are no restrictions on its					

use as long as its content is in no way modified and this statement is not removed.	
EMBL; U68222; AAB53104.1; -; mRNA.	
InterPro; IPR000347; Metallthion_15p.	
Pfam; PF01439; Metallothio_2; 1.	
ProDom; PD001611; Metallthion_15p; 1.	
KW Metal-binding; Metal-thiolate cluster.	
FT NON TER 1	
SQ SEQUENCE 28 AA; 2914 MW; 936F98ADB314F03A CRC64;	
Query Match 15.9%;	Score 21; DB 1; Length 28;
Best Local Similarity 100.0%;	Pred. No. 1.8e+05;
Matches 4;	Conservative 0;
Mismatches 0;	Indels 0;
Gaps 0;	
QY 22 ENDA 25	
Db 10 ENDA 13	
RESULT 43	
VI03_VACCP	STANDARD;
ID VI03_VACCP	PRT;
AC Q00334;	28 AA.
DT 01-APR-1993	(Rel. 25, Created)
DT 01-APR-1993	(Rel. 25, Last sequence update)
DT 13-SEP-2005	(Rel. 48, Last annotation update)
DE Protein I3 (Fragment).	
GN ORFNames=I3L;	
OS Vaccinia virus (strain L-IVP) (VACV).	
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	
OC Orthopoxvirus.	
OX NCBI_TaxID=31531;	
[1]	
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].	
RP MEDLINE=91066899; PubMed=2250685;	
RA Riazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,	
RA Mikriukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,	
RA Malygin E.G.	
RT "Molecular-biological study of vaccinia virus genome. II. Localization	
RT and nucleotide sequence of vaccinia virus genes coding for proteins	
RT 36K and 12K."	
RL Mol. Biol. (Mosk.) 24:968-976 (1990).	
CC -!- MISCELLANEOUS: This protein is synthesized in the early as well as	
CC the late phase of infection.	
CC -!- SIMILARITY: Belongs to the poxviruses I3 family.	
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between the Swiss Institute of Bioinformatics and the EMBL outstation -	
the European Bioinformatics Institute. There are no restrictions on its	
use as long as its content is in no way modified and this statement is not	
removed.	
EMBL; X61165; CAA43473.1; -; Genomic_DNA.	
InterPro; IPR006754; Pox_I3_1_ssdna_bd.	
Pfam; PF04661; Pox_I3_1_	
KW Early protein; Late protein.	
FT NON TER 1	
SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;	
Query Match 15.9%;	Score 21; DB 1; Length 28;
Best Local Similarity 50.0%;	Pred. No. 1.8e+05;
Matches 3;	Conservative 2;
Mismatches 1;	Indels 0;
Gaps 0;	
QY 20 EYENDS 25	
Db 14 EYEDS 19	
RESULT 44	
VIP_CANFA	STANDARD;
ID VIP_CANFA	PRT;
AC P63289; P04565;	28 AA.

```
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
DE polypeptide).
GN Name=VIP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86313167; PubMed=3748846; DOI=10.1016/0196-9781(86)90158-0;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP causes vasodilation, lowers arterial blood pressure,
CC stimulates myocardial contractility, increases glycerolysis and
CC relaxes the smooth muscle of trachea, stomach and gall bladder.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P18509; IGEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Amidation; Direct protein sequencing; Glucagon family; Hormone.
FT MOD_RES 28 28 Asparagine amide.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;
Best Local Similarity 20.8%; Pred. No. 1.8e+05;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKEIDALEYENDAL 26
Db |:::|
4 AVFTDNYTLRKQMAVKYLSIL 27

RESULT 45
ID VIP_CAPHI STANDARD; PRT; 28 AA.
AC P63290; P04565;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Vasoactive intestinal peptide (VIP) (Vasoactive intestinal
DE polypeptide).
GN Name=VIP;
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86313167; PubMed=3748846; DOI=10.1016/0196-9781(86)90158-0;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
```

```
CC -!- FUNCTION: VIP causes vasodilation, lowers arterial blood pressure,
CC stimulates myocardial contractility, increases glycerolysis and
CC relaxes the smooth muscle of trachea, stomach and gall bladder.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P18509; IGEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Amidation; Direct protein sequencing; Glucagon family; Hormone.
FT MOD_RES 28 28 Asparagine amide.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 15.9%; Score 21; DB 1; Length 28;
Best Local Similarity 20.8%; Pred. No. 1.8e+05;
Matches 5; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 3 AALKQKIASLKEIDALEYENDAL 26
Db |:::|
4 AVFTDNYTLRKQMAVKYLSIL 27

Search completed: November 21, 2005, 21:46:22
Job time : 144 secs
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Query Match          34.8%; Score 46; DB 1; Length 28;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 8; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQIEDALE 20
   |:|:::|:|:::|
Db 4 KKLAEKLEKLEKLEKALE 23

RESULT 2
PCT-US92-06412-1
; Sequence 1, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4) 4"
PCT-US92-06412-1

Query Match          34.8%; Score 46; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 6.1;
Matches 8; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQIEDALE 20
   |:|:::|:|:::|
Db 4 KKLAEKLEKLEKLEKALE 23

RESULT 3
US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 5559223
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; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7) 4"
US-08-182-175A-3

Query Match          30.3%; Score 40; DB 1; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKOKIASLKQIEDALE 20
   |:|:::|:|:::|
Db 4 KKLAEKLEKLEKLEKALE 23

RESULT 4
US-08-474-633A-70
; Sequence 70, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND
; TITLE OF INVENTION: METHODS FOR INCREASING
; TITLE OF INVENTION: INCREASING THE LYSINE
; TITLE OF INVENTION: AND THREONINE CONTENT
; TITLE OF INVENTION: OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
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;; CITY: WILMINGTON
;; STATE: DELAWARE
;; COUNTRY: U.S.A.
;; ZIP: 19898
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY DISK
;; OPERATING SYSTEM: IBM PC COMPATIBLE
;; SOFTWARE: MICROSOFT WORD VERSION 2.0C
;; CURRENT APPLICATION DATA:
;; FILING DATE: US/08/474,633A
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BARBARA C. SIEGELL
;; REGISTRATION NUMBER: 30,684
;; REFERENCE/DOCKET NUMBER: BB-1037-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4931
;; TELEFAX: 302-773-0164
;; TELEX: 835420
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..28
;; OTHER INFORMATION: /label= name
;; /note= "(SSP 7)4"
;; US-08-474-633A-70

Query Match 30.3%; Score 40; DB 1; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIADALE 20
|:|::|:|::|:|
Db 4 KKLAMEBKLEKAMEBKLEKAME 23

RESULT 5
US-08-823-771-70
; Sequence 70, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/474,633
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BARBARA C. SIEGELL
;; REGISTRATION NUMBER: 30,684
;; REFERENCE/DOCKET NUMBER: BB-1037-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4931
;; TELEFAX: 302-773-0164
;; TELEX: 835420
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 28 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..28
;; OTHER INFORMATION: /label= name
;; /note= "(SSP 7)4"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
;; US-08-823-771-70

Query Match 30.3%; Score 40; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 42;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIADALE 20
|:|::|:|::|:|
Db 4 KKLAMEBKLEKAMEBKLEKAME 23

RESULT 6
PCT-US92-06412-3
; Sequence 3, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:


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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-18
Query Match      28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 IAAKKQKIASLKQIEDALEYENDALE 27
   : ||| : ||| : ||| : ||| :
DB 3 LKALKKALKKALKKALKKALKKALK 28

RESULT 16
US-08-944-133-31
; Sequence 31, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-944-133-31
Query Match      28.0%; Score 37; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 4 ALKKQKIASLKQIEDALEYENDALEQ 28
   : ||| : ||| : ||| : ||| :
DB 2 ALKKALKKALKKALKKALKKALKK 26

RESULT 17

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US-09-320-424-16
; Sequence 16, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cyfokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-09-320-424-16
Query Match      28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.le-02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy   9 IASLKQEIDALE 20
Db   2 LASRQQLEALQ 13

RESULT 18
US-09-320-424-17
; Sequence 17, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cyfokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-09-320-424-17
Query Match      28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.le-02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy   9 IASLKQEIDALE 20
Db   2 IASIRQQIEAIG 13

US-08-823-771-36
; Sequence 36, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-08-823-771-36
Query Match      28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.le-02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy   1 KTAALKQKIATSLKQEIDALE 20
Db   4 KMKAMEEKWKAMEERKKWAKE 23

RESULT 20
US-08-823-771-40
; Sequence 40, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:

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ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-823-771-40
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KIAALKOKIASLKQSIDALE 20
Db 4 KKKAWEKKKAMEKKKAME 23
RESULT 21
US-08-823-771-56
Sequence 56, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-08-823-771-56
Query Match 28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
Qy 1 KIAALKOKIASLKQSIDALE 20
Db 4 KKKAWEKKKAMEKKKAME 23
RESULT 22
US-08-823-771-67
Sequence 67, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND
METHODS FOR INCREASING
INCREASING THE LYSINE
AND THREONINE CONTENT
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,633
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-823-771-67

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;
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-08-823-771-67

Query Match          28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLQKQIDEALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 23
US-09-825-563-16
; Sequence 16, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-09-825-563-16

Query Match          28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 9 IASLQKQIDEALE 20
Db 2 IASIRQQIEAIQ 13

RESULT 24
US-09-825-563-17
; Sequence 17, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
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;
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-09-825-563-17

Query Match          28.0%; Score 37; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 9 IASLQKQIDEALE 20
Db 2 IASIRQQIEAIQ 13

RESULT 25
PCT-US92-06412-2
; Sequence 2, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA: PCT/US92/06412
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
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LOCATION: 1..28
OTHER INFORMATION: /label= name
OTHER INFORMATION: /note= "(SSP 5)4"
PCT-US92-06412-2

Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 26

PCT-US92-06412-39
Sequence 39, Application PC/TUS9206412

GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006

ATTORNEY/AGENT INFORMATION:

NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-06412-39

Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20
Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 27

PCT-US92-06412-43

Sequence 43, Application PC/TUS9206412

GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler

APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06412
FILING DATE: 19920807
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006

ATTORNEY/AGENT INFORMATION:

NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US92-06412-43

Query Match 28.0%; Score 37; DB 4; Length 28;

Best Local Similarity 25.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKOKIASLKOEIDALE 20

Db 4 KMKAMEEKKMKAMEEKKAME 23

RESULT 28

PCT-US92-06412-47

Sequence 47, Application PC/TUS9206412

GENERAL INFORMATION:

APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06412

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/743,006

FILING DATE: 19920807

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-47

Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
Db 4 KMKAMEEKMKAMEEKAME 23

RESULT 29
US-08-944-133-35
; Sequence 35, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE:
; APPLICATION NUMBER: US/08/232,525
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H
; REGISTRATION NUMBER: 33451
; REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 504 387-3221
; TELEFAX: 504 346-8049
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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US-08-944-133-35
Query Match 27.3%; Score 36; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 2 IAALKQKIASLKQEIDALEYENDAL 26
Db 4 LKALKKALKALKKALKALKAL 28

RESULT 30
US-09-082-279B-19
; Sequence 19, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-19

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY 8 KIASLKQEIDALEYENDALE 27
Db 10 KVKLIKQELD--KYKNVTE 27

RESULT 31
US-09-082-279B-20
; Sequence 20, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-20

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

```

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 3 KVKLIKQELD--KYKNAVTE 20

RESULT 32
US-09-082-279B-21
; Sequence 21, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-21

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 7 KVKLIKQELD--KYKNAVTE 24

RESULT 33
US-08-474-349A-225
; Sequence 225, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-024
; CURRENT APPLICATION DATA:
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-226

Qy 8 KIASLKOEIDALEYENDALE 27
|: :|||:| :||| |
Db 10 KVKLIKQELD--KYKNAVTE 27

RESULT 34
US-08-474-349A-226
; Sequence 226, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-024
; CURRENT APPLICATION DATA:
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-226

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-474-349A-225

Query Match 27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

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Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
      |: :|:|:|:|:|:|:|:|:|
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 35
US-08-474-349A-227
; Sequence 227, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-474-349A-227

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
      |: :|:|:|:|:|:|:|:|:|
Db      7 KVKLIKQELD--KYKNAVTE 24

RESULT 36
US-09-315-304B-19
; Sequence 19, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
      |: :|:|:~|:~|:~|:~|:~|
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 37
US-09-315-304B-20
; Sequence 20, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-20

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

QY      8 KIASLKQEI DALEYENDALE 27
      |: :|:~|:~|:~|:~|:~|
Db      3 KVKLIKQELD--KYKNAVTE 20

RESULT 38
US-09-315-304B-21
; Sequence 21, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-21
```

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; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-21

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKQSDALEYENDALE 27
   | : ||||| : || : |
Db 7 KVKLIKQELD--KYKNAVTE 24

RESULT 39
US-09-834-784-19
; Sequence 19, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKQSDALEYENDALE 27
   | : ||||| : || : |
Db 10 KVKLIKQELD--KYKNAVTE 27

RESULT 40
US-09-834-784-20
; Sequence 20, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly

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; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-20

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKQSDALEYENDALE 27
   | : ||||| : || : |
Db 3 KVKLIKQELD--KYKNAVTE 20

RESULT 41
US-09-834-784-21
; Sequence 21, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-834-784-21

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 8 KIASLKQSDALEYENDALE 27
   | : ||||| : || : |
Db 7 KVKLIKQELD--KYKNAVTE 24

RESULT 42
US-09-515-965A-19
; Sequence 19, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.

```

```
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

RESULT 43
US-09-515-965A-20
; Sequence 20, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-20

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

RESULT 44
US-09-515-965A-21
; Sequence 21, Application US/09515965A
; Patent No. 6623741
; GENERAL INFORMATION:
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; APPLICANT: Antczak, J.
; APPLICANT: Delmedico, M.
; APPLICANT: Erickson, J.
; APPLICANT: Lambert, D.
; APPLICANT: Sista, P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
; TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
; FILE REFERENCE: 7872-073
; CURRENT APPLICATION NUMBER: US/09/515,965A
; CURRENT FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1994
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; OTHER INFORMATION: Core polypeptide
US-09-515-965A-21

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 24

RESULT 45
US-09-350-641C-19
; Sequence 19, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-19

Query Match      27.3%; Score 36; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy      8 KIASLKQEIDALEYENDALE 27
      |: :|||:| :|||
Db     10 KVKLIKQELD--KYKNAVTE 27

Search completed: November 21, 2005, 21:41:31
Job time : 31.5 secs
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:41:39 ; Search time 106.5 Seconds
(without alignments)
109.852 Million cell updates/sec

Title: US-10-088-417A-1

Perfect score: 132

Sequence: 1 KIAALKQKIASLKQEDALEYENDALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 5696

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

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2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	43.2	28	4	US-10-360-053-23
2	54	40.9	28	4	US-10-360-053-22
3	51	38.6	28	3	US-09-320-907B-6
4	51	38.6	28	4	US-10-447-232-6
5	45	34.1	28	4	US-10-360-053-21
6	40	30.3	28	4	US-10-023-066A-70
7	40	30.3	28	5	US-10-804-678-70
8	39	29.5	28	5	US-10-830-959-6
9	37	28.0	28	4	US-10-023-066A-36
10	37	28.0	28	4	US-10-023-066A-40
11	37	28.0	28	4	US-10-023-066A-56
12	37	28.0	28	4	US-10-023-066A-67
13	37	28.0	28	4	US-10-652-244-16
14	37	28.0	28	4	US-10-652-244-17
15	37	28.0	28	5	US-10-804-678-36
16	37	28.0	28	5	US-10-804-678-40
17	37	28.0	28	5	US-10-804-678-56
18	37	28.0	28	5	US-10-804-678-67
19	37	28.0	28	5	US-10-900-399-16
20	37	28.0	28	5	US-10-900-399-17
21	36	27.3	28	4	US-10-351-641-19
22	36	27.3	28	4	US-10-351-641-20
23	36	27.3	28	4	US-10-351-641-21
24	36	27.3	28	5	US-10-950-010-331
25	35	26.5	28	4	US-10-267-682-85
26	35	26.5	28	4	US-10-267-748-85
27	35	26.5	28	5	US-10-706-275-6

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28 34 25.8 28 3 US-09-945-917-23 Sequence 23, Appl
29 33 25.0 28 4 US-10-023-066A-58 Sequence 58, Appl
30 33 25.0 28 5 US-10-804-678-58 Sequence 58, Appl
31 32 24.2 28 3 US-09-739-907-173 Sequence 173, Appl
32 32 24.2 28 3 US-09-945-917-24 Sequence 24, Appl
33 32 24.2 28 3 US-09-938-671-173 Sequence 173, Appl
34 32 24.2 28 4 US-10-080-608A-2 Sequence 2, Appl
35 32 24.2 28 4 US-10-370-685-91 Sequence 91, Appl
36 32 24.2 28 4 US-10-267-682-86 Sequence 86, Appl
37 32 24.2 28 4 US-10-267-748-86 Sequence 86, Appl
38 32 24.2 28 5 US-10-851-691-10 Sequence 10, Appl
39 32 24.2 28 5 US-10-935-098-173 Sequence 173, Appl
40 32 24.2 28 5 US-10-892-981A-10 Sequence 10, Appl
41 31 23.5 28 3 US-09-864-761-44899 Sequence 44899, A
42 30 22.7 28 3 US-09-864-761-42292 Sequence 42292, A
43 30 22.7 28 4 US-10-351-641-18 Sequence 18, Appl
44 30 22.7 28 5 US-10-862-195-1275 Sequence 1275, Ap
45 29.5 22.3 28 4 US-10-351-641-77 Sequence 77, Appl

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ALIGNMENTS

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RESULT 1
US-10-360-053-23
; Sequence 23, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-23
Query Match 43.2%; Score 57; DB 4; Length 28;
Best Local Similarity 60.0%; Pred. No. 4;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 KIAALKQKIASLKQEDALE 20
| | | | | | | | | | | | | |
Db 5 KQAAIKNEIAAIAKQIAAIE 24

RESULT 2
US-10-360-053-22
; Sequence 22, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antibo
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376

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; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-22

Query Match      40.9%; Score 54; DB 4; Length 28;
Best Local Similarity 55.0%; Pred. No. 4.9;
Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIADALEYENDALE 20
   |||:|:|:|:|:|:|:|:|:|:|
Db 5 KIAAIEKIAIEEETAAQE 24

RESULT 3
US-09-320-907B-6
; Sequence 6, Application US/09320907B
; Publication No. US20020198360A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/09/320,907B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-320-907B-6

Query Match      38.6%; Score 51; DB 3; Length 28;
Best Local Similarity 40.7%; Pred. No. 12;
Matches 11; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIADALEYENDALE 27
   ||:|:|:|:|:|:|:|:|:|:|
Db 1 KLEALEGRDLDALEGLKLEALEGLDALE 27

RESULT 4
US-10-447-292-6
; Sequence 6, Application US/10447292
; Publication No. US20030224453A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/10/447,292
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/320,907B
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-447-292-6

Query Match      38.6%; Score 51; DB 4; Length 28;
Best Local Similarity 40.7%; Pred. No. 12;
Matches 11; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIADALEYENDALE 27
   ||:|:|:|:|:|:|:|:|:|:|
Db 1 KLEALEGRDLDALEGLKLEALEGLDALE 27

RESULT 5
US-10-360-053-21
; Sequence 21, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenthal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antiboc
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-21

Query Match      34.1%; Score 45; DB 4; Length 28;
Best Local Similarity 56.2%; Pred. No. 72;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEI 16
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Db 12 EIAAIKDKIAAIKEYI 27

RESULT 6
US-10-023-066A-70
; Sequence 70, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; APPLICANT: COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; TITLE OF INVENTION: INCREASING THE LYSINE AND
; TITLE OF INVENTION: THREONINE CONTENT OF THE SEEDS OF
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: E. I. DU PONT DE NEMOURS
; ADDRESSSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-023-066A-70

Query Match 30.3%; Score 40; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 7
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
; INCREASING THE LYSINE CONTENT OF
; THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
```

```
;
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match 30.3%; Score 40; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALE 20
Db 4 KLKAMEEKLKAMEEKLKAME 23

RESULT 8
US-10-830-959-6
; Sequence 6, Application US/10830959
; Publication No. US20040259201A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Howard
; APPLICANT: Nadesalingam, Palaniyar
; APPLICANT: Reid, Kenneth
; APPLICANT: Strong, Peter
; TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
; FILE REFERENCE: 18396/2402
; CURRENT APPLICATION NUMBER: US/10/830,959
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: PCT/GB02/04824
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: GB 0125638.7
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0209619.6
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-830-959-6

Query Match 29.5%; Score 39; DB 5; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQEIDALE 20
Db 2 VASLFQQVEALQ 13

RESULT 9
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
```

```
/
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 10
US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 10
US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-023-066A-40
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQEIDALE 20
|:|::|:|::|:|
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 11
US-10-023-066A-56
; Sequence 56, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND
; COMPANY
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE AND
/ THREONINE CONTENT OF THE SEEDS OF
/ PLANTS
/
/ NUMBER OF SEQUENCES: 107
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS
/ AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MICROSOFT WORD VERSION 2.0C
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,066A
/ FILING DATE: 29-Apr-2002
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56
Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56
Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQSIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 12
US-10-023-066A-67
; Sequence 67, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 5)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-023-066A-67
Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQSIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56
Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQSIDALE 20
Db 4 KMKAMEEKMKAMEEKMKAME 23

RESULT 13
US-10-652-244-16
; Sequence 16, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-652-244-16
Query Match      28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQSIDALE 20
Db 2 IASLKQSIDALE 13

RESULT 14
US-10-652-244-17
; Sequence 17, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
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US-10-652-244-17

Query Match 28.0%; Score 37; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IASLKQEIDALE 20
|:|:|:|:|:|:|:
Db 2 IASIROQIEAIQ 13

RESULT 15

US-10-804-678-36
; Sequence 36, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:

APPLICANT: EPELBAUM, SABINE URSULA

FALCO, SAVERIO CARL

MCDEVITT, RAYMOND ERVIN, III

TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT OFFICE 97

SOFTWARE: MICROSOFT WINDOWS 95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678

FILING DATE: 19-Mar-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/049,304

FILING DATE: 27-Mar-1998

APPLICATION NUMBER: 08/824,627

FILING DATE: MARCH 27, 1997

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNNE M.

REGISTRATION/DOCKET NUMBER: BB-1037-F

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-5481

TELEFAX: 302-892-7949

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-10-804-678-36

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALE 20
|:|:|:|:|:|:|:
Db 4 KMKAMEEKKMKAMEKKAME 23

RESULT 16

US-10-804-678-40
; Sequence 40, Application US/10804678

; Publication No. US20050005330A1

; GENERAL INFORMATION:

APPLICANT: EPELBAUM, SABINE URSULA

FALCO, SAVERIO CARL

MCDEVITT, RAYMOND ERVIN, III

TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT OFFICE 97

SOFTWARE: MICROSOFT WINDOWS 95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678

FILING DATE: 19-Mar-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/049,304

FILING DATE: 27-Mar-1998

APPLICATION NUMBER: 08/824,627

FILING DATE: MARCH 27, 1997

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNNE M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1037-F

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-5481

TELEFAX: 302-892-7949

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-10-804-678-40

Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 25.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQEIDALE 20
|:|:|:|:|:|:|:
Db 4 KMKAMEEKKMKAMEKKAME 23

RESULT 17

US-10-804-678-56

; Sequence 56, Application US/10804678

; Publication No. US20050005330A1

; GENERAL INFORMATION:

APPLICANT: EPELBAUM, SABINE URSULA

FALCO, SAVERIO CARL

MCDEVITT, RAYMOND ERVIN, III

TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

Db 2 IASLRQQLAQLQ 13

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RESULT 20
US-10-900-399-17
; Sequence 17, Application US/10900399
; Publication No. US20050158823A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-17
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Query Match 28.0%; Score 37; DB 5; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

QY 9 IASLRQQLAQLQ 20
Db 2 IASLRQQLAQLQ 13

```
RESULT 21
US-10-351-641-19
; Sequence 19, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Core polypeptide
US-10-351-641-19
```

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Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;
```

QY 8 KIASLKQEI DALEYENDALE 27
Db 10 KVKLIKQELD--KYKNAVTE 27

```
RESULT 22
US-10-351-641-20
; Sequence 20, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-20
```

```
Query Match 27.3%; Score 36; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 1e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 2; Gaps 1;
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QY 8 KIASLKQEI DALEYENDALE 27
Db 3 KVKLIKQELD--KYKNAVTE 20

```
RESULT 23
US-10-351-641-21
; Sequence 21, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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[illegible]

TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-023-066A-58

Query Match 25.0%; Score 33; DB 4; Length 28;
Best Local Similarity 20.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQKIDALE 20
Db 4 KMKAMEEKLKMKKEEKLKQME 23

RESULT 30

US-10-804-678-58
Sequence 58, Application US/10804678
Publication No. US20050005330A1

GENERAL INFORMATION:

APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE CONTENT OF
THE SEEDS OF PLANTS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT OFFICE 97
SOFTWARE: MICROSOFT WINDOWS 95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/804,678
FILING DATE: 19-Mar-2004
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/049,304
FILING DATE: 27-Mar-1998
APPLICATION NUMBER: 08/824,627
FILING DATE: MARCH 27, 1997

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1037-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-892-7949
TELEX: 835420

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-10-804-678-58
Query Match 25.0%; Score 33; DB 5; Length 28;
Best Local Similarity 20.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KIAALKQKIASLKQKIDALE 20
Db 4 KMKAMEEKLKMKKEEKLKQME 23

RESULT 31

US-09-739-907-173
Sequence 173, Application US/09739907
Patent No. US20010012889A1

GENERAL INFORMATION:

APPLICANT: ROSEN ET AL.
TITLE OF INVENTION: 36 Human Secreted Proteins
FILE REFERENCE: P2022P1
CURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,567
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 173
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens

US-09-739-907-173

Query Match 24.2%; Score 32; DB 3; Length 28;
Best Local Similarity 35.7%; Pred. No. 3.4e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KQKIASLKQKIDAL 19
Db 13 EKIEDISNKVDAM 26

RESULT 32

US-09-945-917-24
Sequence 24, Application US/09945917
Publication No. US20030042381A1

GENERAL INFORMATION:

APPLICANT: Bogaert, Thierry
APPLICANT: Vandekerckhove, Joel
TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
THEIR PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
USE IN THE CONTROL OF CELL BEHAVIOUR
FILE REFERENCE: P/14-1
CURRENT APPLICATION NUMBER: US/09/945,917
CURRENT FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 24
LENGTH: 28
TYPE: PRT
ORGANISM: Caenorhabditis elegans

US-09-945-917-24

Query Match 24.2%; Score 32; DB 3; Length 28;
Best Local Similarity 46.7%; Pred. No. 3.4e+03;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 5 LKQKIASLKQKIDAL 19
Db 8 LKTENKQKKEVDKL 22

RESULT 35
US-10-370-685-91
; Sequence 91, Application US/10370685
; Publication No. US20030215903A1

LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-10-267-682-86

Query Match 24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAALKOKIASLKQE 15
DB 1 IARLEEKVKTLKAQ 14

RESULT 37
US-10-267-748-86
Sequence 86, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 863-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Query Match 24.2%; Score 32; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IAALKOKIASLKQE 15
DB 1 IARLEEKVKTLKAQ 14

RESULT 38
US-10-851-691-10
Sequence 10, Application US/10851691
Publication No. US20050009988A1
GENERAL INFORMATION:
APPLICANT: HARRIS, J. MILTON
APPLICANT: KOZLOWSKI, ANTONI
APPLICANT: MCMAHUS, SAMUEL P.
APPLICANT: BENTLEY, MICHAEL A.
APPLICANT: CHARLES, STEPHEN A.

TITLE OF INVENTION: POLYMER DERIVATIVES HAVING PARTICULAR ATOM ARRANGEMENTS
FILE REFERENCE: SHE0071.00
CURRENT APPLICATION NUMBER: US/10/851,691
CURRENT FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: 60/493,213
PRIOR FILING DATE: 2003-05-23
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic polypeptide
US-10-851-691-10

Query Match 24.2%; Score 32; DB 5; Length 28;
Best Local Similarity 27.3%; Pred. No. 3.4e+03;
Matches 6; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 3 AALKOKIASLKQEIADALEYEND 24
DB 4 AVTENYTKLRKQLAKKYLND 25

RESULT 39
US-10-935-098-173
Sequence 173, Application US/10935098
Publication No. US20050042667A1
GENERAL INFORMATION:
APPLICANT: Lafleur et al.
FILE REFERENCE: P2022P1C3
CURRENT APPLICATION NUMBER: US/10/935,098
CURRENT FILING DATE: 2004-09-08
PRIOR APPLICATION NUMBER: 09/938,671
PRIOR FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/739,907
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: PCT/US99/00108
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/070,657
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,704
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 173
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens

PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42292
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008392.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
US-09-864-761-42292
Query Match 22.7%; Score 30; DB 3; Length 28;
Best Local Similarity 31.6%; Pred. No. 6.2e+03;
Matches 6; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
Qy 10 ASLKQEIADALEYENDALEQ 28
Db 9 AQVQAEIEELQETQALDK 27
RESULT 43
US-10-351-641-18
Sequence 18, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1757
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-10-351-641-18
Query Match 22.7%; Score 30; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.2e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 8 KIASLKQEI 17
Db 17 KVKLIKQELD 26
RESULT 44
US-10-862-195-1275
Sequence 1275, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:
APPLICANT: GYGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1275
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments
OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1275
Query Match 22.7%; Score 30; DB 5; Length 28;
Best Local Similarity 53.8%; Pred. No. 6.2e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 15 EIDALEYENDALE 27
Db 4 ELDAYEAEGLAD 16
RESULT 45
US-10-351-641-77
Sequence 77, Application US/10351641
Publication No. US20030186874A1
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
FILE REFERENCE: 7872-100
CURRENT APPLICATION NUMBER: US/10/351,641
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 09/350,641
PRIOR FILING DATE: 1999-07-09

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; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-77
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Query Match      22.3%; Score 29.5; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.2e+03;
Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
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QY      10 ASLKQEIDAL-EYENDAL 26
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Db       5 AQLQFTYDLKDYINDAL 22
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Search completed: November 21, 2005, 22:04:03
Job time : 107.5 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:46:35 ; Search time 4 seconds
(without alignments)

7.909 Million cell updates/sec

Title: US-10-088-417a-1

Perfect score: 132

Sequence: 1 KIAALQKIASLQKQIDALEYENDALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 45

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgm2_6/ptodata/2/pubaa/US10_NEW_PUB pep.*
- 2: /cgm2_6/ptodata/2/pubaa/US06_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/2/pubaa/US07_NEW_PUB pep.*
- 4: /cgm2_6/ptodata/2/pubaa/US08_NEW_PUB pep.*
- 5: /cgm2_6/ptodata/2/pubaa/US09_NEW_PUB pep.*
- 6: /cgm2_6/ptodata/2/pubaa/PCT_NEW_PUB pep.*
- 7: /cgm2_6/ptodata/2/pubaa/US11_NEW_PUB pep.*
- 8: /cgm2_6/ptodata/2/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	18.2	28	1	US-10-939-890-382
2	24	18.2	28	1	US-10-939-890-698
3	21	15.9	28	7	US-11-019-894A-21
4	19	14.4	28	1	US-10-939-890-325
5	19	14.4	28	1	US-10-939-890-346
6	19	14.4	28	1	US-10-939-890-355
7	19	14.4	28	1	US-10-939-890-383
8	19	14.4	28	1	US-10-939-890-699
9	19	14.4	28	1	US-10-939-890-822
10	19	14.4	28	1	US-10-939-890-831
11	18.5	14.0	28	1	US-10-939-890-385
12	18.5	14.0	28	1	US-10-939-890-701
13	18	13.6	28	1	US-10-997-201A-13
14	17	12.9	28	1	US-10-632-349-4
15	17	12.9	28	1	US-10-939-890-464
16	17	12.9	28	1	US-10-939-890-720
17	17	12.9	28	1	US-10-939-890-723
18	17	12.9	28	7	US-11-021-441-50
19	16	12.1	28	1	US-10-983-464-22
20	14	10.6	28	1	US-10-939-890-326
21	13	9.8	28	1	US-10-939-890-356
22	13	9.8	28	1	US-10-939-890-384
23	13	9.8	28	1	US-10-939-890-630
24	13	9.8	28	1	US-10-939-890-719
25	13	9.8	28	1	US-10-939-890-721

Sequence 722, App
Sequence 794, App
Sequence 795, App
Sequence 832, App
Sequence 847, App
Sequence 236, App
Sequence 820, App
Sequence 344, App
Sequence 353, App
Sequence 474, App
Sequence 726, App
Sequence 829, App
Sequence 351, App
Sequence 827, App
Sequence 3, Appli
Sequence 294, App
Sequence 10, Appl
Sequence 213, App
Sequence 345, App
Sequence 821, App

26 13 9.8 28 1 US-10-939-890-722
27 13 9.8 28 1 US-10-939-890-794
28 13 9.8 28 1 US-10-939-890-795
29 13 9.8 28 1 US-10-939-890-832
30 13 9.8 28 1 US-10-939-890-847
31 13 9.8 28 7 US-11-022-562-236
32 12.5 9.5 28 1 US-10-939-890-344
33 12.5 9.5 28 1 US-10-939-890-820
34 12 9.1 28 1 US-10-939-890-353
35 12 9.1 28 1 US-10-939-890-474
36 12 9.1 28 1 US-10-939-890-726
37 12 9.1 28 1 US-10-939-890-829
38 11 8.3 28 1 US-10-939-890-351
39 11 8.3 28 1 US-10-939-890-827
40 11 8.3 28 7 US-11-109-161-3
41 9 6.8 28 1 US-10-986-501-294
42 9 6.8 28 1 US-10-716-189-10
43 9 6.8 28 7 US-11-096-706-213
44 8 6.1 28 1 US-10-939-890-345
45 8 6.1 28 1 US-10-939-890-821

ALIGNMENTS

RESULT 1
US-10-939-890-382
; Sequence 382, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 28
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-382

Query Match 18.2%; Score 24; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 19 LEYEND 24
: ||| ||
Db 4 IEYVND 9

RESULT 2

US-10-939-890-698
; Sequence 698, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US09

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 698

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-698

Query Match 18.2%; Score 24; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 19 LEYEND 24
: ||| ||
Db 4 IEYVND 9

RESULT 3

US-11-019-894A-21

; Sequence 21, Application US/11019894A

; Publication No. US20050245451A1

; GENERAL INFORMATION:

; APPLICANT: Pincus, Matthew R.

; TITLE OF INVENTION: PEPTIDES SELECTIVELY LETHAL TO THE MALIGNANT AND TRANSFORMED

; FILE REFERENCE: 1181-17 CIP A

; CURRENT APPLICATION NUMBER: US/11/019,894A

; CURRENT FILING DATE: 2004-12-21

; PRIOR APPLICATION NUMBER: 10/386,737

; PRIOR FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: 09/827,683

; PRIOR FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,102

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: 60/363,785

; PRIOR FILING DATE: 2002-03-12

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 21

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: peptide; Human C-JUN membrane penetrating leader sequence

US-11-019-894A-21

Query Match 15.9%; Score 21; DB 7; Length 28;

Best Local Similarity 35.7%; Pred. No. 3.5e+02;

Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KIAALKQKIASLKQ 14

Db 12 RIAASKRRKKLER 25

RESULT 4

US-10-939-890-325

; Sequence 325, Application US/10939890

; Publication No. US20050250700A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.

; APPLICANT: Sexton, Daniel J.

; APPLICANT: Dransfield, Daniel T.

; APPLICANT: Ladner, Robert C.

; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussat, Philippe

; APPLICANT: Fan, Hong

; APPLICANT: Khurana, Sudha

; APPLICANT: Linder, Karen E.

; APPLICANT: Marinelli, Edmund R.

; APPLICANT: Nanjappan, Palaniappa

; APPLICANT: Nunn, Adrian D.

; APPLICANT: Pillai, Radhakrishna

; APPLICANT: Pochon, Sibylle

; APPLICANT: Ramalingam, Kondareddiar

; APPLICANT: Shrivastava, Ajay

; APPLICANT: Song, Bo

; APPLICANT: Swenson, Rolf E.

; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US09

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

```
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-325

Query Match      14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      14 QETDAL 19
Db      16 QRVDSL 21

RESULT 5
US-10-939-890-346
; Sequence 346, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 346
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-346

Query Match      14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;

US-10-939-890-346

; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-355

Query Match      14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      17 DALE 20
Db      3 DALE 6

RESULT 6
US-10-939-890-355
; Sequence 355, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-355

Query Match      14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      20 EYENDALEQ 28
Db      2 QWESDYWDQ 10

RESULT 7
US-10-939-890-383
; Sequence 383, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
```

```

; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 383
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-383

```

```

Query Match          14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      17 DALE 20
        ||||
Db       3 DALE 6

```

```

RESULT 8
US-10-939-890-699
; Sequence 699, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```

```

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)-(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-699

```

```

Query Match          14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      17 DALE 20
        ||||
Db       3 DALE 6

```

```

RESULT 9
US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731

```

;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/440,411
;; PRIOR FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: US 60/360,851
;; PRIOR FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 883
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 822
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide

;; NAME/KEY: MOD_RES
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: ACETYLTATION
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (9)..(9)
;; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (28)..(28)
;; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-822

Query Match 14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 DALE 20
|||
Db 3 DALE 6

RESULT 10

US-10-939-890-831
;; Sequence 831, Application US/10939890
;; Publication No. US20050250700A1
;; GENERAL INFORMATION:
;; APPLICANT: Sato, Aaron K.
;; APPLICANT: Sexton, Daniel J.
;; APPLICANT: Dransfield, Daniel T.
;; APPLICANT: Ladner, Robert C.
;; APPLICANT: Arbogast, Christophe
;; APPLICANT: Bussat, Philippe
;; APPLICANT: Fan, Hong
;; APPLICANT: Khurana, Sudha
;; APPLICANT: Linder, Karen E.
;; APPLICANT: Marinelli, Edmund R.
;; APPLICANT: Nanjappan, Palaniappa
;; APPLICANT: Nunn, Adrian D.
;; APPLICANT: Pillai, Radhakrishna
;; APPLICANT: Pochon, Sibylle
;; APPLICANT: Ramalingam, Kondareddiar
;; APPLICANT: Shrivastava, Ajay
;; APPLICANT: Song, Bo
;; APPLICANT: Swenson, Rolf E.
;; APPLICANT: Von Wronski, Mathew A.
;; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;; FILE REFERENCE: D0617.70014US00
;; CURRENT APPLICATION NUMBER: US/10/939,890
;; CURRENT FILING DATE: 2004-09-13
;; PRIOR APPLICATION NUMBER: US 10/661,156
;; PRIOR FILING DATE: 2003-09-11
;; PRIOR APPLICATION NUMBER: US 10/382,082
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: PCT/US03/06731
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/440,411
;; PRIOR FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: US 60/360,851

;; PRIOR FILING DATE: 2002-03-01
;; NUMBER OF SEQ ID NOS: 883
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 831
;; LENGTH: 28
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; OTHER INFORMATION: Synthetic peptide

;; NAME/KEY: MOD_RES
;; LOCATION: (1)..(1)
;; OTHER INFORMATION: ACETYLTATION
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (16)..(16)
;; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (21)..(21)
;; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (28)..(28)
;; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker

US-10-939-890-831

Query Match 14.4%; Score 19; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 6.3e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 20 EYENDALEQ 28
:::|:|:|
Db 2 QWESDYWDQ 10

RESULT 11

US-10-939-890-385
;; Sequence 385, Application US/10939890
;; Publication No. US20050250700A1
;; GENERAL INFORMATION:
;; APPLICANT: Sato, Aaron K.
;; APPLICANT: Sexton, Daniel J.
;; APPLICANT: Dransfield, Daniel T.
;; APPLICANT: Ladner, Robert C.
;; APPLICANT: Arbogast, Christophe
;; APPLICANT: Bussat, Philippe
;; APPLICANT: Fan, Hong
;; APPLICANT: Khurana, Sudha
;; APPLICANT: Linder, Karen E.
;; APPLICANT: Marinelli, Edmund R.
;; APPLICANT: Nanjappan, Palaniappa
;; APPLICANT: Nunn, Adrian D.
;; APPLICANT: Pillai, Radhakrishna
;; APPLICANT: Pochon, Sibylle
;; APPLICANT: Ramalingam, Kondareddiar
;; APPLICANT: Shrivastava, Ajay
;; APPLICANT: Song, Bo
;; APPLICANT: Swenson, Rolf E.
;; APPLICANT: Von Wronski, Mathew A.
;; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
;; FILE REFERENCE: D0617.70014US00
;; CURRENT APPLICATION NUMBER: US/10/939,890
;; CURRENT FILING DATE: 2004-09-13
;; PRIOR APPLICATION NUMBER: US 10/661,156
;; PRIOR FILING DATE: 2003-09-11
;; PRIOR APPLICATION NUMBER: US 10/382,082
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: PCT/US03/06731
;; PRIOR FILING DATE: 2003-03-03
;; PRIOR APPLICATION NUMBER: US 60/440,411
;; PRIOR FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: US 60/360,851

```
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-385

Query Match      14.0%; Score 18.5; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 7.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY      13 KQEDAL-EYENDA 25
       :||| | | :|||
Db      7 QERDKLREHYDDA 20

RESULT 12
US-10-939-890-701
; Sequence 701, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (26)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-701

Query Match      14.0%; Score 18.5; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 7.3e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY      13 KQEDAL-EYENDA 25
       :||| | | :|||
Db      7 QERDKLREHYDDA 20

RESULT 13
US-10-997-201A-13
; Sequence 13, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-13

Query Match      13.6%; Score 18; DB 1; Length 28;
Best Local Similarity 60.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      7 QKIAS 11
       :|||
Db      11 EKVAS 15

RESULT 14
US-10-632-349-4
; Sequence 4, Application US/10632349
; Publication No. US20050250685A1
; GENERAL INFORMATION:
; APPLICANT: ZAVERI, CHANDA
; TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY
; FILE REFERENCE: 37896.00002.DIV3
; CURRENT APPLICATION NUMBER: US/10/632,349
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 09/879,666
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/211,859
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Acetylation
US-10-632-349-4

Query Match      12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      12 LKQEIDALE 20
```



```
Db      ||::: :|
        16 LKEKEVVE 24

RESULT 15
US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 464
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-464

Query Match      12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      14 QEIDALEY 21
Db      6 QDMIRLDY 13

RESULT 16
US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
```

```
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617 70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 893
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 723
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ NAME/KEY: MOD RES
/ LOCATION: (1)-(1)
/ OTHER INFORMATION: ACETYLATION
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)-(28)
/ OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-723

Query Match      12.9%; Score 17; DB 1; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      14 QEIDALEY 21
Db      6 QDMRLDY 13

RESULT 18
US-11-021-441-50
/ Sequence 50, Application US/11021441
/ Publication No. US20050249748A1
/ GENERAL INFORMATION:
/ APPLICANT: DUBENSKY, Thomas W., Jr.
/ APPLICANT: PORTNOY, Daniel A.
/ APPLICANT: LUCKETT, William S., Jr.
/ APPLICANT: COOK, David N.
/ TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
/ TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 282172003900
/ CURRENT APPLICATION NUMBER: US/11/021,441
/ CURRENT FILING DATE: 2004-12-23
/ PRIOR APPLICATION NUMBER: US 60/616,750
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/615,287
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER: US 60/599,377
/ PRIOR FILING DATE: 2004-08-05
/ PRIOR APPLICATION NUMBER: PCT/US2004/23881
/ PRIOR FILING DATE: 2004-07-23
/ PRIOR APPLICATION NUMBER: US 10/883,599
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: US 60/556,744
/ PRIOR FILING DATE: 2004-03-26
/ NUMBER OF SEQ ID NOS: 129

/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Bacillus anthracis
US-11-021-441-50

Query Match      12.9%; Score 17; DB 7; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      6 KOKIAS 11
Db      3 KUKMAS 8

RESULT 19
US-10-983-464-22
/ Sequence 22, Application US/10983464
/ Publication No. US20050245446A1
/ GENERAL INFORMATION:
/ APPLICANT: Hailes, Helen C.
/ APPLICANT: Tabor, Alethea B.
/ APPLICANT: Wong, John B.
/ APPLICANT: Pilkington-Wiksa, Michael
/ APPLICANT: Hart, Stephen L.
/ APPLICANT: Hurley, Christopher A.
/ TITLE OF INVENTION: Materials For The Delivery of
/ TITLE OF INVENTION: Biologically-Active Material To Cells
/ FILE REFERENCE: 50318/008001
/ CURRENT APPLICATION NUMBER: US/10/983,464
/ CURRENT FILING DATE: 2004-11-08
/ PRIOR APPLICATION NUMBER: PCT/GB03/01985
/ PRIOR FILING DATE: 2003-05-08
/ PRIOR APPLICATION NUMBER: US 60/576,270
/ PRIOR FILING DATE: 2004-06-02
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-983-464-22

Query Match      12.1%; Score 16; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      6 KOKIASLKOE 15
Db      13 KKKKGACRRE 22

RESULT 20
US-10-939-890-326
/ Sequence 326, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buseat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
```

Tue Nov 22 08:14:35 2005

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; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356

```

Query Match 10.6%; Score 14; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QEI 16
 DB 10 QEI 12

```

RESULT 21
US-10-939-890-356
; Sequence 356, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03

```

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; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356

```

Query Match 9.8%; Score 13; DB 1; Length 28;
 Best Local Similarity 22.2%; Pred. No. 1.1e+03;
 Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASLKQEI 16
 DB 8 EILSMADQL 16

```

RESULT 22
US-10-939-890-384
; Sequence 384, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-09-11
; PRIOR FILING DATE: 2003-03-03
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-384

```

Query Match 9.8%; Score 13; DB 1; Length 28;
 Best Local Similarity 28.6%; Pred. No. 3.1e+03;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 20 EYNDAL 26
: : | |
Db 2 QWYDGL 8

RESULT 23

US-10-939-890-630
; Sequence 630, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 630

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a JJ spacer linker

US-10-939-890-630

Query Match 9.8%; Score 13; DB 1; Length 28;

Best Local Similarity 22.2%; Pred. No. 3.1e+03;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASLKQEI 16
: | : :
Db 8 EILSMADQL 16

RESULT 24

US-10-939-890-719
; Sequence 719, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 719

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; FEATURE:

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-719

Query Match 9.8%; Score 13; DB 1; Length 28;

Best Local Similarity 22.2%; Pred. No. 3.1e+03;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 KIASLKQEI 16
: | : :
Db 8 EILSMADQL 16

RESULT 25

US-10-939-890-721

; Sequence 721, Application US/10939890

; Publication No. US20050250700A1

GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 721
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a iv-Dde linker
US-10-939-890-721

Query Match 9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KIASLKQEI 16
Db 8 EILSMADQL 16

RESULT 26
US-10-939-890-722
Sequence 722, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-01-15
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 722
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-722

Query Match 9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 KIASLKQEI 16
Db 8 EILSMADQL 16

RESULT 27
US-10-939-890-794
Sequence 794, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

```
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 794
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)..(28)
/ OTHER INFORMATION: Lys residue modified with SATA linker
US-10-939-890-794
```

```
Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      8 KIASLKQEI 16
      |||||
Db       8 EILSMADQL 16
```

```
RESULT 28
US-10-939-890-795
/ Sequence 795, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 832
```

```
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 795
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: ACETYLATION
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (28)..(28)
/ OTHER INFORMATION: Lys residue modified with SATA JJ spacer linker
US-10-939-890-795
```

```
Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      8 KIASLKQEI 16
      |||||
Db       8 EILSMADQL 16
```

```
RESULT 29
US-10-939-890-832
/ Sequence 832, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 832
```

```
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (26)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-832

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      8 KIASLKQEI 16
Db      8 EILSMADQL 16

RESULT 30
US-10-939-890-847
; Sequence 847, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 847
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
```

```
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a J spacer linker
US-10-939-890-847

Query Match          9.8%; Score 13; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 3.1e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      8 KIASLKQEI 16
Db      8 EILSMADQL 16

RESULT 31
US-11-022-562-236
; Sequence 236, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-236

Query Match          9.8%; Score 13; DB 7; Length 28;
Best Local Similarity 12.5%; Pred. No. 3.1e+03;
Matches 1; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      12 LKQEIDAL 19
Db      8 MPQDLNTM 15

RESULT 32
US-10-939-890-344
; Sequence 344, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
```

```
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344
```

```
Query Match          9.5%; Score 12.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      13 KQRIDALEY 21
Db      3 KKE-DAQQW 10
```

```
RESULT 33
US-10-939-890-820
; Sequence 820, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 820
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD_RES
; LOCATION: (3)..(4)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-820
```

```
Query Match          9.5%; Score 12.5; DB 1; Length 28;
Best Local Similarity 44.4%; Pred. No. 3.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      13 KQRIDALEY 21
Db      3 KKE-DAQQW 10
```

```
RESULT 34
US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 353
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
```



```
;
;
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

Query Match          9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 19 LEYENDALEQ 28
Db 12 LNYRPTMFHQ 21

RESULT 35
US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726

Query Match          9.1%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 14 QEIDAL 19
Db 14 QAEDSL 19

RESULT 37
US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
```

```

; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-829

```

Query Match 9.1%; Score 12; DB 1; Length 28;
 Best Local Similarity 30.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 19 LEYENDALEQ 28
Db 12 LNVKPTMFHQ 21

```

```

RESULT 38
US-10-939-890-351
; Sequence 351, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle

```

```

; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351

```

Query Match 8.3%; Score 11; DB 1; Length 28;
 Best Local Similarity 66.7%; Pred. No. 4.5e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 23 NDA 25
Db 17 DDA 19

```

```

RESULT 39
US-10-939-890-827
; Sequence 827, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411

```

```

; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)-(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827

Query Match      8.3%; Score 11; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 NDA 25
Db 17 DDA 19

RESULT 40
US-11-109-161-3
; Sequence 3, Application US/11109161
; Publication No. US20050244422A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; APPLICANT: SINGH, Baljit K.
; TITLE OF INVENTION: METHODS FOR DELIVERING MED
; TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
; TITLE OF INVENTION: STRESS
; FILE REFERENCE: 51490-20003.00
; CURRENT APPLICATION NUMBER: US/11/109,161
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,141
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/563,676
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/657,826
; PRIOR FILING DATE: 2005-03-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-109-161-3

Query Match      8.3%; Score 11; DB 7; Length 28;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KOK 8
Db 6 KKK 8

RESULT 41
US-10-986-501-294
; Sequence 294, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 294
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-294

Query Match      6.8%; Score 9; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QKI 9
Db 10 QRL 12

RESULT 42
US-10-716-189-10
; Sequence 10, Application US/10716189
; Publication No. US20050249750A1
; GENERAL INFORMATION:
; APPLICANT: Nardin, Elizabeth
; APPLICANT: Moreno, Alberto
; TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
; FILE REFERENCE: 5986/1B615-US1
; CURRENT APPLICATION NUMBER: US/10/716,189
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/060,450
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: 60/033,916
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of Carboxyl Terminus of SEQ ID NO:4 to
; OTHER INFORMATION: Amino Terminus of Seq ID NO: 1, designated T1B
US-10-716-189-10

Query Match      6.8%; Score 9; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      16 ID 17
       :|
Db      20 VD 21

RESULT 43
US-11-096-706-213
; Sequence 213, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-00822005
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (DNA binding domain)
US-11-096-706-213

Query Match      6.8%; Score 9; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      23 NDAL 26
       :|
Db      13 SDHL 16

RESULT 44
US-10-939-890-345
; Sequence 345, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION

; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-345

Query Match      6.1%; Score 8; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 6.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      19 LEY 21
       :|
Db      19 LFY 21

RESULT 45
US-10-939-890-821
; Sequence 821, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
```

```
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-821
```

```
Query Match      6.1%; Score 8; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 6.3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      19 LEY 21
      |||
Db      19 LFY 21
```

Search completed: November 21, 2005, 22:04:16
Job time : 4.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:38; Search time 130 Seconds
(without alignments)
94.635 Million cell updates/sec

Title: US-10-088-417A-4

Perfect score: 137
Sequence: 1 KIRALKWKNHLKQETAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 9880

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database: A Geneseq 21:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*
 - 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	137	100.0	28	AAB74346	Peptide S
2	137	100.0	28	AAB74347	Peptide S
3	124	90.5	28	AAB74349	Peptide S
4	123	89.8	28	AAB74348	Peptide S
5	123	89.8	28	AAB74356	Peptide S
6	123	89.8	28	AAB74352	Peptide S
7	122	89.1	28	AAB74345	Peptide S
8	105	76.6	28	ADM41438	Self-asse
9	81	59.1	28	ABR84737	DE novo d
10	75	54.7	28	AAB74343	Peptide S
11	75	54.7	28	AAB74351	Peptide S
12	75	54.7	28	ADM41436	Self-asse
13	74	54.0	28	AAB74341	Peptide S
14	74	54.0	28	AAB74342	Peptide S
15	70	51.1	28	AAB74355	Peptide u
16	70	51.1	28	AAB74350	Peptide S
17	59	43.1	28	ABR84735	DE novo d
18	54	39.4	28	ABR84736	DE novo d
19	45	32.8	28	AAU14021	Peptide s
20	45	32.8	28	ABO10240	Heptad re
21	45	32.8	28	ADB67071	Canonical
22	45	32.8	28	ADL99341	Nanostroc
23	44	32.1	28	AAR31979	SSP4 poly
24	42	30.7	28	ADY52134	Heparin b

Ady52132 Heparin b
Aab50879 Integrin
Aab59138 Alpha-hel
Adl15278 Prion pro
Aar31981 SSP7 poly
Aar78256 SSP(7)4 h
Ada15966 Synthetic
Abo44343 Ear I-bas
Adw71693 Peptide S
Aar34576 Domain 1
Aar32693 SSP polyp
Aar3689 SSP polyp
Aar31980 SSP5 poly
Aar78255 SSP(S)4 h
Aar78250 SSP 5.5.5
Aar78244 SSP 5.5.5
Aar78242 SSP 5.5.5
Aaw62935 Minialis
Aaw60508 Synthetic
Aaw60516 Synthetic
Aaw60510 Synthetic

ALIGNMENTS

RESULT 1
AAB74346
ID AAB74346 standard; peptide; 28 AA.

XX AAB74346;
AC
XX
XX
DT 02-JUL-2001 (first entry)
XX
DE Peptide SAF-p2B.
XX
XX Atomic Force Microscopy; AFM.
XX
OS Unidentified.
XX
XX WO200121646-A1.
XX
XX 29-MAR-2001.
XX
XX 18-SEP-2000; 2000WO-GB003576.
XX
XX 17-SEP-1999; 99GB-00022013.
XX
XX (UVSU-) UNIV SUSSEX.
XX
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX
XX Disclosure; Page 9; 45pp; English.
XX
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is the peptide monomer unit SAF-p2B
XX
XX Sequence 28 AA;

Query Match 100.0%; Score 137; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 3.7e-11; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

Oy 1 KIRALKWKNHLKQETAALEQ 28

[illegible]

XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
PT tissue engineering, or constructing nanoscale molecular sieves.
PT
XX
XX Disclosure; Page 9; 45pp; English.
PS

OS Unidentified.
 XX WO200121646-A1.
 XX 29-MAR-2001.
 XX PD
 XX PF 18-SEP-2000; 2000WO-GB003576.
 XX PR 17-SEP-1999; 99GB-00022013.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX DR
 XX PT New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX PS Claim 16; Page 26; 45pp; English.
 XX CC The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-plc
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX
 OY 1 KIRALKWNAHLKQEIADALEYENDALEQ 28
 |||||
 DB 1 KIRALKQKIASLKQEIADALEYENDALEQ 28
 |||||
 RESULT 11
 AAB74351
 ID AAB74351 standard; peptide; 28 AA.
 XX AC AAB74351;
 XX DT 02-JUL-2001 (first entry)
 XX DE Peptide SAF-pl.
 XX KW Atomic Force Microscopy; AFM.
 XX OS Unidentified.
 XX WO200121646-A1.
 XX PD 29-MAR-2001.
 XX PF 18-SEP-2000; 2000WO-GB003576.
 XX PR 17-SEP-1999; 99GB-00022013.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX WPI; 2001-335468/35.
 XX DR
 XX PT New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX PS Claim 16; Page 26; 45pp; English.
 XX
 CC The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-pl
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 4; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX
 OY 1 KIRALKWNAHLKQEIADALEYENDALEQ 28
 |||||
 DB 1 KIRALKQKIASLKQEIADALEYENDALEQ 28
 |||||
 RESULT 12
 ADM41436
 ID ADM41436 standard; peptide; 28 AA.
 XX AC ADM41436;
 XX DT 03-JUN-2004 (first entry)
 XX DB Self-assembling peptide fibre SAF-pl.
 XX KW Fibre-shaping peptide; self-assembling peptide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal NH3 moiety"
 XX WO2004022584-A1.
 XX PD 18-MAR-2004.
 XX PF 08-SEP-2003; 2003WO-GB003900.
 XX PR 06-SEP-2002; 2002GB-00020805.
 XX PA (UYSU-) UNIV SUSSEX.
 XX PI Woolfson D, Ryadnov MG;
 XX WPI; 2004-248444/23.
 XX DR
 XX PT Novel fiber-shaping peptide comprising hub and several peptide monomer
 PT units, useful for producing protein structure useful in purification of
 PT biological fluids and in surface engineering procedures.
 XX PS Example 30; Page 22; 37pp; English.
 XX CC The present sequence is that of self-assembling peptide fibre (SAF) SAF-
 CC pl. The invention relates to fibre-shaping (Fish) peptides ADM41434-
 CC ADM41435 that are capable of interacting with SAFs to form protein
 CC structures. The Fish peptides allow morphological changes (branches,
 CC splits, kinks and bends) to be made to protein fibres comprising SAFs. By
 CC incorporating such morphological changes in the protein fibres, it is
 CC possible to generate a variety of (nanoscale) protein structures, such as
 CC assemblies in general, including matrix, filter, network, grid and
 CC scaffold structures. Use of the protein structures in the purification of
 CC biological fluids, for assembling cells for cell and tissue engineering,
 CC and in surface engineering procedures is claimed.
 XX SQ Sequence 28 AA;
 Query Match 54.7%; Score 75; DB 8; Length 28;
 Best Local Similarity 71.4%; Pred. No. 0.0069;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 XX

```

QY 1 KIRALKWNAHLKQETAALEQ 28
Db 1 KIAALKQKIAHLKQETAALEQ 28

RESULT 13
AAB74341
ID AAB74341 standard; peptide; 28 AA.
XX AC AAB74341;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-plA.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Page 9; 45pp; English.
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is the peptide monomer unit SAF-plA
XX Sequence 28 AA;

Query Match 54.0%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0094;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 28
Db 1 KIAALKQKIAHLKQETAALEQ 28

RESULT 15
AAB74355
ID AAB74355 standard; peptide; 28 AA.
XX AC AAB74355;
XX 02-JUL-2001 (first entry)
XX Peptide used to form blunt-ended heterodimers.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.
XX 18-SEP-2000; 2000WO-GB003576.
XX 17-SEP-1999; 99GB-00022013.
XX (UYSU-) UNIV SUSSEX.
XX Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
XX WPI; 2001-335468/35.
XX New protein structures with peptide monomer units, useful in Atomic Force
XX Microscopy, purifying biological fluids, promoting tissue repair and
XX tissue engineering, or constructing nanoscale molecular sieves.
XX Disclosure; Fig 8; 45pp; English.
XX The present invention relates to a protein structure with several first
XX peptide monomer units arranged in a first strand and several second
XX peptide monomer units arranged in a second strand. The structure is
XX useful in Atomic Force Microscopy and a number of other applications. The
XX present sequence is a peptide used to form blunt-ended heterodimers.
XX Sequence 28 AA;

Query Match 54.0%; Score 74; DB 4; Length 28;
Best Local Similarity 71.4%; Pred. No. 0.0094;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 28
Db 1 KIAALKQKIAHLKQETAALEQ 28

RESULT 14
AAB74342
ID AAB74342 standard; peptide; 28 AA.
XX AC AAB74342;
XX 02-JUL-2001 (first entry)
XX Peptide SAF-plB.
XX Atomic Force Microscopy; AFM.
XX Unidentified.
XX WO200121646-A1.
XX 29-MAR-2001.

```

XX SQ Sequence 28 AA;

Query Match 51.1%; Score 70; DB 4; Length 28;
 Best Local Similarity 53.6%; Pred. No. 0.032;
 Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKOEIAALEQIEIALEQ 28
 Db 1 EIDALEYENDALEQKIALKOKIASLQ 28

RESULT 16
 AAB74350
 ID AAB74350 standard; peptide; 28 AA.
 XX
 AC AAB74350;
 DT 02-JUL-2001 (first entry)
 XX
 DE Peptide SAF-p3.
 XX
 KW Atomic Force Microscopy; AFM.
 XX
 OS Unidentified.
 XX
 FN WO200121646-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 18-SEP-2000; 2000WO-GB003576.
 XX
 PR 17-SEP-1999; 99GB-00022013.
 XX
 PA (UYSU-) UNIV SUSSEX.
 XX
 PI Woolfson DN, Walshaw J, Pandya MJ, Colyer J;
 XX
 DR WPI; 2001-335468/35.
 XX
 PT New protein structures with peptide monomer units, useful in Atomic Force
 PT Microscopy, purifying biological fluids, promoting tissue repair and
 PT tissue engineering, or constructing nanoscale molecular sieves.
 XX
 PS Disclosure; Page 12; 45pp; English.
 XX
 CC The present invention relates to a protein structure with several first
 CC peptide monomer units arranged in a first strand and several second
 CC peptide monomer units arranged in a second strand. The structure is
 CC useful in Atomic Force Microscopy and a number of other applications. The
 CC present sequence is the peptide monomer unit SAF-p3
 XX
 SQ Sequence 28 AA;

Query Match 51.1%; Score 70; DB 4; Length 28;
 Best Local Similarity 53.6%; Pred. No. 0.032;
 Matches 15; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKOEIAALEQIEIALEQ 28
 Db 1 EIDALEYENDALEQKIALKOKIASLQ 28

RESULT 17
 ABR84735
 ID ABR84735 standard; peptide; 28 AA.
 XX
 AC ABR84735;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE DE novo designed AHEC peptide #3.
 XX

KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
 KW AHEC; antiparallel; drug targeting.
 XX
 OS Synthetic.
 XX
 FN WO2003066660-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 05-FEB-2003; 2003WO-EP001217.
 XX
 PR 05-FEB-2002; 2002US-0354376P.
 XX
 PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
 XX
 PI Caterer NR, Uttental LO, Neilson RW;
 XX
 DR WPI; 2003-679535/64.
 XX
 CC Composition useful for forming therapeutic antibodies and antibody
 CC fragments comprises pair of antibody Fv fragments linked and stabilized
 CC by antiparallel heterogeneous alpha-helical coiled-coil peptides.
 XX
 PS Disclosure; Page 14; 35pp; English.
 XX
 CC The present invention relates to a composition which comprises a pair of
 CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
 CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
 CC form multimeric complexes and therapeutic antibodies and antibody
 CC fragments useful for e.g. inhibition of receptor binding and the
 CC targeting of drugs, toxins and labels in research, industry and
 CC healthcare. The present sequence is an AHEC peptide used in the
 CC exemplification of the invention
 XX
 SQ Sequence 28 AA;

Query Match 43.1%; Score 59; DB 7; Length 28;
 Best Local Similarity 40.0%; Pred. No. 0.94;
 Matches 10; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKWNAHLKOEIAALEQIEIALEQ 28
 Db 1 AIEYEQAALKEIEIAIKDKIAAIKE 25

RESULT 18
 ABR84736
 ID ABR84736 standard; peptide; 28 AA.
 XX
 AC ABR84736;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE DE novo designed AHEC peptide #4.
 XX
 KW Antibody Fv chain; stabilisation; assembly; alpha-helical coiled-coil;
 KW AHEC; antiparallel; drug targeting.
 XX
 OS Synthetic.
 XX
 FN WO2003066660-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 05-FEB-2003; 2003WO-EP001217.
 XX
 PR 05-FEB-2002; 2002US-0354376P.
 XX
 PA (IMMU-) IMMUNOLEX THERAPEUTICS APS.
 XX
 PI Caterer NR, Uttental LO, Neilson RW;
 XX
 DR WPI; 2003-679535/64.

XX Composition useful for forming therapeutic antibodies and antibody
PT fragments comprises pair of antibody Fv fragments linked and stabilized
by antiparallel heterogeneous alpha-helical coiled-coil peptides.

PS Disclosure; Page 14; 35pp; English.

CC The present invention relates to a composition which comprises a pair of
CC antibody Fv fragments linked and stabilised by antiparallel heterogeneous
CC alpha-helical coiled-coil (AHEC) peptides. The composition is used to
CC form multimeric complexes and therapeutic antibodies and antibody
CC fragments useful for e.g. inhibition of receptor binding and the
CC targeting of drugs, toxins and labels in research, industry and
CC healthcare. The present sequence is an AHEC peptide used in the
CC exemplification of the invention

XX Sequence 28 AA;

SQ Query Match 39.4%; Score 54; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KIRALKWKNVHLKQEITAALEOEIA 24
|||:::||::|||||::|:
Db 5 KIAATBEIKTAQBEEITAQAQEEKIA 28

RESULT 19
AAU14021
ID AAU14021 standard; peptide; 28 AA.
AC AC
AD AD
AE AE
AF AF
AG AG
AH AH
AI AI
AJ AJ
AK AK
AL AL
AM AM
AN AN
AO AO
AP AP
AQ AQ
AR AR
AS AS
AT AT
AU AU
AV AV
AW AW
AX AX
AY AY
AZ AZ
BA BA
BB BB
BC BC
BD BD
BE BE
BF BF
BG BG
BH BH
BI BI
BJ BJ
BK BK
BL BL
BM BM
BN BN
BO BO
BP BP
BQ BQ
BR BR
BS BS
BT BT
BU BU
BV BV
BW BW
BX BX
BY BY
ZZ ZZ

CC repeat containing peptide from a non-HIV source used to compile the
 CC motifs
 XX
 SQ Sequence 28 AA;
 Query Match 32.8%; Score 45; DB 6; Length 28;
 Best Local Similarity 42.9%; Pred. No. 70;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 KIRALKWNAHLKOEIAALEQ 21
 Db 7 KVEELLSKNYHLENEVARLKK 27
 RESULT 21
 ADB67071
 ID ADB67071 standard; peptide; 28 AA.
 AC ADB67071;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Canonical leucine zipper GCN4 peptide SEQ ID NO:90.
 XX
 KW staged assembly; nanostructure; peptide nucleic acid; PNA;
 KW structural reinforcement; aerogel; paper; plastic; cement;
 KW tensile strength; identification marker; anti-counterfeiting marker;
 KW enzyme support; catalyst support; assembly scaffold; nanowire;
 KW nanocircuit; molecular sieve; molecular filter; biosensor.
 XX
 OS Synthetic.
 OS Saccharomyces cerevisiae.
 XX
 PN WO2003072829-A1.
 XX
 PD 04-SEP-2003.
 XX
 XX 21-FEB-2003; 2003WO-US005390.
 XX
 XX 21-FEB-2002; 2002US-00080608.
 XX
 XX (NANO-) NANOFAMES INC.
 XX
 XX Hyman PL, Goldberg EB;
 XX
 XX WPI; 2003-721788/68.
 XX
 PT Staged assembly of nanostructures, useful e.g. in biosensors or as
 PT catalyst supports, using assembly units derived from peptide nucleic
 PT acids.
 XX
 PS Disclosure; Page 29; 118pp; English.
 XX
 CC The present invention describes a method (M1) for the staged assembly of
 CC a nanostructure using peptide nucleic acids (PNAs). M1 comprises: (a)
 CC contacting a nanostructure intermediate (NSI) having at least one unbound
 CC joining element (JE) with an assembly unit (AU) that comprises several
 CC different JE where: (i) none of these JE can interact with itself or
 CC other JE; and (ii) only one JE in AU and a single unbound JE in NSI are
 CC complementary, so that AU becomes non-covalently linked to NSI to produce
 CC a new NSI for use in subsequent cycles; (b) removing unbound AU; and (c)
 CC cyclic repetition of (a) and (b) to form a nanostructure. The new feature
 CC is that the complementary JE in at least one cycle are PNAs. Also
 CC described are nanostructures formed from many AU, comprising different
 CC JE, where at least one AU includes PNA. M1 is useful for producing
 CC nanostructures with a very wide range of potential applications, e.g.
 CC structural reinforcements (for aerogels, paper, plastics or cement,
 CC particularly as long fibres to improve tensile strength); identification
 CC (anti-counterfeiting) markers; enzyme or catalyst supports; assembly
 CC scaffolds; for construction of nanowires or nanocircuits; size markers
 CC for electron microscopy; molecular sieves or filters; substrates for
 CC optical and other surface coatings; scaffolds for solubilising enzymes or
 CC for trapping, protecting and delivering specific molecules; in high-

CC density computer memories; as artificial zeolite for absorbing ions from
 CC water and for construction of new materials, including use in biosensors.
 CC PNAs are more homogeneous than inorganic nanoparticles generally used to
 CC form nanostructures, so will produce structures with predictable geometry
 CC and stoichiometry. The present sequence represents a canonical leucine
 CC zipper and high stability dimerisation sequence peptide, which is used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 28 AA;
 Query Match 32.8%; Score 45; DB 7; Length 28;
 Best Local Similarity 42.9%; Pred. No. 70;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 KIRALKWNAHLKOEIAALEQ 21
 Db 7 KVEELLSKNYHLENEVARLKK 27
 RESULT 22
 ADL99341
 ID ADL99341 standard; peptide; 28 AA.
 XX
 AC ADL99341;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Nanostructure assembly peptide #24.
 XX
 KW peptide nucleic acid; PNA; nanostructure.
 XX
 OS Synthetic.
 XX
 PN US20032215903-A1.
 XX
 PD 20-NOV-2003.
 XX
 XX 21-FEB-2003; 2003US-00370685.
 XX
 XX 21-FEB-2002; 2002US-00080608.
 XX
 XX (HYMA/) HYMAN P L.
 XX (GOLD/) GOLDBERG E B.
 XX
 XX Hyman PL, Goldberg EB;
 XX
 XX WPI; 2004-021840/02.
 XX
 PT Staged assembly of a nanostructure containing peptide nucleic acid
 PT assembly units comprising contacting a nanostructure intermediate with an
 PT assembly unit comprising different joining elements, and removing unbound
 PT assembly units.
 XX
 PS Disclosure; Page 11; 73pp; English.
 XX
 CC The invention relates to staged assembly of a nanostructure comprising:
 CC (a) contacting a nanostructure intermediate comprising at least one
 CC unbound joining element with an assembly unit comprising different
 CC joining elements; (b) removing unbound assembly units; and (c) repeating
 CC steps (a)-(b) for a sufficient number of cycles to form a nanostructure,
 CC where the assembly unit in at least one cycle comprises a peptide nucleic
 CC acid. A single joining element of the different joining elements and a
 CC single unbound joining element of the nanostructure intermediate are
 CC complementary joining elements, where the assembly unit is non-covalently
 CC bound to the nanostructure intermediate to form a new nanostructure
 CC intermediate for use in subsequent cycles. The method for staged assembly
 CC of a nanostructure further comprises: (i) capping the nanostructure with
 CC at least one capping unit; and (ii) post-assembly conversion of specific
 CC non-covalent interactions of complementary joining elements to covalent
 CC linkages, where the linkages are stabilised. The nanostructure
 CC intermediate comprises a surface bound initiator assembly unit. A first
 CC assembly unit used in at least one cycle comprises at least one
 CC structural element covalently linked to a first joining element

AC ADY52132;
 XX 19-MAY-2005 (first entry)
 XX Heparin binding protein associated amino acid sequence, SEQ ID NO:65.
 XX heparin binding protein; assay; heparin; anticoagulant; blood-clotting.
 XX heparin binding protein; assay; heparin; anticoagulant; blood-clotting.
 XX Unidentified.
 XX WO2005018552-A2.
 XX 03-MAR-2005.
 XX 12-AUG-2004; 2004WO-US026066.
 XX 12-AUG-2003; 2003US-0494495P.
 XX (UTAH) UNIV UTAH RES FOUND.
 XX Prestwich GD, Shenshen C, Beattie J, Mostert MJ;
 XX WPI; 2005-214150/22.
 XX New composition comprising a heparin binding molecule (HBM) having a
 XX heparin binding unit (HBU), useful in neutralizing heparin in a subject.
 XX Disclosure; SEQ ID NO 65; 152pp; English.
 XX The invention relates to a new composition comprising a heparin binding
 XX molecule (HBM) having a heparin binding unit (HBU). Also described are
 XX (i) a nucleic acid comprising a sequence encoding a heparin-binding
 XX molecule (HBM) nucleic acid, (ii) an assay for detecting heparin, (iii) a
 XX method for determining the amount of heparin in a sample, (iv) a method
 XX of detecting heparin, (v) a method of removing heparin from a sample,
 XX (vi) a method for detecting heparin on coated surfaces, (vii) a kit
 XX comprising a HBM, color developing reagent, control standards, wash
 XX buffer and instructions, (viii) an apparatus comprising a medical device
 XX coated with HBM, (ix) a method of manufacturing a medical device, and (x)
 XX a method of neutralizing heparin in a subject. The composition further
 XX comprises a linker and a second HBU and a second linker and a third HBU.
 XX The heparin-binding unit comprises a peptide having at least 80% identity
 XX to a fully defined sequence 62-amino acid sequence (SEQ ID NO: 6). The
 XX first, second and third HBU comprise a fully defined 9-amino acid
 XX sequence (SEQ ID NO: 1). The HBM is fused to a bacterial glutathione-S-
 XX transferase (GST). The GST-HBM is also fused to a bacterial alkaline
 XX phosphatase (BAP). The GST-HBM is also fused to an enhanced green
 XX fluorescent protein (EGFP). The composition is useful in neutralizing
 XX heparin in a subject. This sequence represents an amino acid sequence
 XX relating to the present invention.
 XX Sequence 28 AA;
 Query Match 29.9%; Score 41; DB 9; Length 28;
 Best Local Similarity 33.3%; Pred. No. 2.4e+02;
 Matches 8; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 5 LKWNALHKOETAAAEQ 28
 Db 3 LKDNSQLKSEVSKLSQLVKKQ 26
 RESULT 26
 AAB50879
 ID AAB50879 standard; peptide; 28 AA.
 XX AC
 XX AAB50879;
 XX 19-MAR-2001 (first entry)
 XX Integrin cytoplasmic domain heptad-repeat.
 XX Integrin; transmembrane protein; alpha4 integrin inhibitor; paxillin;
 XX

KW immunosuppressive; inflammatory bowel disease; arthritis;
 KW multiple sclerosis; asthma; atherosclerosis; wound healing;
 XX cytoplasmic domain; heptad-repeat.
 OS Homo sapiens.
 XX WO200073342-A1.
 PN 07-DEC-2000.
 PD 01-JUN-2000; 2000WO-US015153.
 PF 01-JUN-1999; 99US-00323447.
 PR (SCRI) SCRIPPS RES INST.
 XX Ginsberg MH, Pfaff M, Liu S;
 XX WPI; 2001-070959/08.
 XX Polypeptides useful in construction of structural models for identifying
 XX therapeutic compounds, comprises series of heptad repeats that mimic a
 XX transmembrane domain and cytoplasmic domain attached to heptad repeats.
 XX Example 2; Fig 1A; 37pp; English.
 XX The present sequence is given in a specification relating to a
 XX polypeptide comprising a series of heptad-repeats that mimic a
 XX transmembrane domain, and a selected cytoplasmic domain attached to the
 XX heptad repeats. At least a portion of the polypeptide is prepared
 XX recombinantly or at least 1 heptad repeat in the series has a different
 XX amino acid sequence to other heptad repeats in the series. The
 XX polypeptide is useful in the construction of structural models which are
 XX useful for evaluating structure and activity of a selected cytoplasmic domain
 XX clustered transmembrane protein having the selected cytoplasmic domain
 XX and for identifying therapeutic compounds. It is also useful for
 XX identifying agents as inhibitors of alpha4 integrin biological responses
 XX by contacting the structural model with paxillin or a paxillin related
 XX molecule in the presence and absence of a test agent and determining
 XX binding of paxillin or paxillin related molecule to the structural model.
 XX A decrease in binding in the presence of the test agent indicates that
 XX the test agent is an inhibitor of alpha4 integrin biological response.
 XX Inhibitors of the binding of paxillin to alpha4 are useful in blocking
 XX immune responses in conditions such as inflammatory bowel disease,
 XX arthritis, multiple sclerosis and asthma and in inhibiting
 XX atherosclerosis and scarring during wound healing
 XX Sequence 28 AA;
 Query Match 28.5%; Score 39; DB 4; Length 28;
 Best Local Similarity 37.0%; Pred. No. 4.4e+02;
 Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 1 KIRALKWNAHLKOEIAAEQIAALE 27
 Db 1 KLEALEGRDLDALEKLEALEKGLDALE 27
 RESULT 27
 AAB59138
 ID AAB59138 standard; peptide; 28 AA.
 XX AC
 XX AAB59138;
 XX 21-MAR-2001 (first entry)
 XX Alpha-helical heptad repeat.
 XX Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
 XX thrombosis; malignancy.
 XX Synthetic.
 XX


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Query Match      27.7%; Score 38; DB 6; Length 28;
Best Local Similarity 24.0%; Pred. No. 6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKOEIAALEOEIAA 25
Db 4 KUKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 32
ABO44343
ID ABO44343 standard; peptide; 28 AA.
XX
AC ABO44343;
XX
DT 25-SEP-2003 (first entry)
XX
DE Ear 1-based lysine-rich heptad repeat SSP(7)4.
XX
KW Aspartokinase; AKIII; dihydrodipicolinic acid synthase; DHDPS;
KW seed lysine content; seed threonine content; seed storage protein; SSP;
KW chloroplast transit sequence; lysine-rich protein;
KW lysine ketoglutarate reductase; LKR; transgenic.
XX
OS Synthetic.
XX
PN US2003056242-A1.
XX
PD 20-MAR-2003.
XX
PF 17-DEC-2001; 2001US-00023066.
XX
PR 19-MAR-1992; 92US-00855414.
PR 18-MAR-1993; 93WO-US002480.
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 24-MAR-1997; 97US-00823771.
XX
PA (FALC/) FALCO S C.
XX
PI Falco SC;
XX
DR WPI; 2003-521869/49.
DR N-PSDB; ACH03709.
XX
PT New nucleic acid fragment encoding aspartokinase and dihydrodipicolinic
PT acid synthase, useful for increasing threonine or lysine content of seeds
PT of plant.
XX
PS Example 21; Page 44; 116pp; English.
XX
CC The invention relates to an isolated nucleic acid fragment comprising a
CC first nucleic acid subfragment encoding aspartokinase (AK) that is
CC substantially insensitive to inhibition by lysine, and a second nucleic
CC acid subfragment encoding dihydrodipicolinic acid synthase (DHDPS) that
CC is substantially insensitive to inhibition by lysine. Also included are
CC an isolated nucleic acid fragment comprising a nucleic acid subfragment
CC encoding lysine ketoglutarate reductase (LKR), a chimaeric gene (where
CC the nucleic acid fragment is operably linked to a plant chloroplast
CC transit sequence and to a seed-specific regulatory sequence, a plant
CC comprising the nucleic acid/chimaeric gene in its genome, a seed obtained
CC from the plant, increasing threonine or lysine content of the seeds of
CC plant, a plant capable of transmitting the chimaeric gene to a progeny of
CC plant having the ability to produce levels of free threonine or lysine at
CC least two times greater than the free threonine levels of untransformed
CC plants, a transformed (soybean) plant comprising seeds that accumulate
CC lysine at a level at least ten percent to four-fold higher than the seeds
CC of an untransformed plant, a transformed rapeseed comprising seeds that
CC accumulate lysine to a level between ten percent and one hundred percent
CC higher than that of the seeds of an untransformed plant, a monocot plant
CC comprising in its genome the nucleic acid fragment having the monocot-
CC embryo specific promoter and a transformed corn plant comprising seeds
CC that accumulate lysine to a level between ten percent and one hundred
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CC thirty percent higher than the seeds of the untransformed plant. Also
CC disclosed are synthetic lysine-rich seed storage proteins (SSP), built up
CC from monomer lysine-rich heptad repeats (encoded by EarI restriction
CC enzyme-based oligonucleotides) used as a pool of lysine in a transformed
CC plant. The nucleic acid fragments, genes and methods are useful for
CC increasing threonine or lysine content of the seeds of the plant. Seeds
CC containing increased threonine or lysine content eliminate the need to
CC supplement mixed grain feeds with lysine or threonine produced via
CC microbial fermentation. The present sequence is a lysine-rich heptad
CC repeat for use as a monomer unit in a synthetic seed storage protein
XX
SQ Sequence 28 AA;
```

```
Query Match      27.7%; Score 38; DB 6; Length 28;
Best Local Similarity 24.0%; Pred. No. 6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 KIRALKKNAHLKOEIAALEOEIAA 25
Db 4 KUKAMEEKLKAMEEKLKAMEEKLKA 28
```

```
RESULT 33
ADW71693
ID ADW71693 standard; peptide; 28 AA.
XX
AC ADW71693;
XX
DT 24-MAR-2005 (first entry)
XX
DE Peptide SSP(7)4 SEQ ID NO:70.
XX
KW transgenic plant; amino acid production; seed; enzyme engineering.
XX
OS Synthetic.
XX
PN US2005005330-A1.
XX
PD 06-JAN-2005.
XX
PF 19-MAR-2004; 2004US-00804678.
XX
PR 06-JAN-1994; 94US-00178212.
PR 07-JUN-1995; 95US-00474633.
PR 27-MAR-1997; 97US-00824627.
PR 27-MAR-1998; 98US-00049304.
XX
PA (FALC/) FALCO S C.
PA (MCDE/) MCDEVITT R E.
PA (EPBL/) EPBLBAUM S U.
XX
PI Falco SC, Mcdevitt RE, Epelbaum SU;
XX
DR WPI; 2005-065280/07.
DR N-PSDB; ADW71691.
XX
PT New isolated lysine ketoglutarate reductase/saccharopine dehydrogenase
PT nucleic acid fragment, useful for increasing levels of lysine in the
PT seeds of transformed plants.
XX
PS Example 21; SEQ ID NO 70; 142pp; English.
```

```
XX
CC The invention relates to a novel isolated nucleic acid sequence which is
CC useful in antisense inhibition or sense suppression of endogenous lysine
CC ketoglutarate reductase/saccharopine dehydrogenase activity in a corn
CC plant or corn plant cell, where the isolated nucleic acid fragment
CC comprises all or a part of a nucleic acid sequence (ADW71743). The
CC isolated nucleic acid fragment is useful for increasing levels of lysine
CC in the seeds of transformed plants. The present sequence represents a
CC peptide encoded by an oligonucleotide used to create chimeric genes of
CC the invention.
XX
SQ Sequence 28 AA;
```

Query Match 27.7%; Score 38; DB 9; Length 28;
 Best Local Similarity 24.0%; Pred. No. 6e+02;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Oy 1 KIRALKWKNHLKQEIALLQEIATA 25
 Db 4 KIKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 34
 AAR34576
 ID AAR34576 standard; protein; 28 AA.
 XX AC AAR34576;
 XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 04-JUN-1993 (first entry)
 XX Domain 1 from integrase like protein Rci.
 XX cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG;
 KW Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis;
 KW malaria; influenza virus; CTL; herpes virus.
 XX Borrelia burgdorferi.
 XX WO9307897-A1.
 XX 29-APR-1993.
 XX 21-OCT-1992; 92WO-US009075.
 XX 21-OCT-1991; 91US-00780261.
 XX (MEDI-) MEDIMUNE INC.
 XX Stover CK;
 XX WPI; 1993-152187/18.
 XX Expression vector for expressing protein or polypeptide in mycobacterium
 PT - contg DNA sequences encoding lipoprotein secretion signal and peptide
 PT heterologous to bacteria expressing fusion protein of lipoprotein
 PT heterologous to bacteria.
 XX Disclosure; Fig 29; 86pp; English.

XX This sequence is domain 1 from the integrase like protein Rci. The whole
 CC coding sequence of the enzyme could be included in an expression vector
 CC in order to aid its integration into its host. The expression vector also
 CC includes at least the secretion signal of a lipoprotein and a second
 CC sequence encoding a heterologous protein and a mycobacterial promoter to
 CC control expression of the heterologous protein. (Updated on 09-JAN-2003
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 28 AA;

Query Match 27.0%; Score 37; DB 2; Length 28;
 Best Local Similarity 56.2%; Pred. No. 8.1e+02;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 11 HLKQEIALLQEIATA 26
 Db 5 HLALETAMRQEIALL 20

RESULT 35
 AAR32693
 ID AAR32693 standard; protein; 28 AA.
 XX AAR32693;
 AC AAR32693;

XX 25-MAR-2003 (revised)
 DT 22-JUN-1993 (first entry)
 XX SSP polypeptide produced from clone 84-H3.
 DE Heptad; plants; custom tailored storage proteins; in vivo; expression.
 XX Heptad; plants; custom tailored storage proteins; in vivo; expression.
 XX Synthetic.
 XX WO9303160-A1.
 XX 18-FEB-1993.
 XX 07-AUG-1992; 92WO-US006412.
 XX 09-AUG-1991; 91US-00743006.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Falco SC, Keeler SJ, Rice JA;
 XX WPI; 1993-076517/09.
 DR N-PSDB; AAQ37274.
 XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
 PT vivo in plants to serve as custom-tailored storage proteins with
 PT specified aminoacid content.
 XX Disclosure; Page 124; 176pp; English.
 XX The sequence represents a synthetic heptad polypeptide which can be
 CC expressed in vivo in plants to serve as a synthetic seed storage protein
 CC which can be custom-tailored for specific end-user requirements. The DNA
 CC encoding the heptad may be used to transform plants to increase the
 CC content of partic. amino acids such as lysine or methionine in seeds or
 CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX Sequence 28 AA;

Query Match 26.3%; Score 36; DB 2; Length 28;
 Best Local Similarity 24.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Oy 1 KIRALKWKNHLKQEIALLQEIATA 25
 Db 4 KIKAMEEKLKAMEEKLKAMEEKLKA 28

RESULT 36
 AAR32689
 ID AAR32689 standard; peptide; 28 AA.
 XX AAR32689;
 AC AAR32689;
 DT 25-MAR-2003 (revised)
 DT 22-JUN-1993 (first entry)
 XX SSP polypeptide produced from clone D16.
 DE Heptad; plants; custom tailored storage proteins; in vivo; expression.
 XX Heptad; plants; custom tailored storage proteins; in vivo; expression.
 XX Synthetic.
 XX WO9303160-A1.
 XX 18-FEB-1993.
 XX 07-AUG-1992; 92WO-US006412.
 XX 09-AUG-1991; 91US-00743006.
 XX

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PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1993-076517/09.
DR N-PSDB; AAQ37270.
XX
XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
PS Disclosure; Page 120; 176pp; English.
XX
CC The sequence represents a synthetic heptad polypeptide which can be
CC expressed in vivo in plants to serve as a synthetic seed storage protein
CC which can be custom-tailored for specific end-user requirements. The DNA
CC encoding the heptad may be used to transform plants to increase the
CC content of partic amino acids such as lysine or methionine in seeds or
CC leaves. See also AAR31979-86 and AAR32659-705. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWKNVHLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::|::|::|::|::|::|::|

RESULT 37
AAR31980
ID AAR31980 standard; peptide; 28 AA.
XX
AC AAR31980;
XX
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1993 (first entry)
XX
XX SSP5 polypeptide, suitable for in vivo expression.
XX
XX Heptad; plants; custom tailored storage proteins.
XX
XX Synthetic.
XX
XX OS
XX WO9303160-A1.
XX
XX PD 18-FEB-1993.
XX
XX PF 07-AUG-1992; 92WO-US006412.
XX
XX PR 09-AUG-1991; 91US-00743006.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Keeler SJ, Rice JA;
XX
XX WPI; 1993-076517/09.
XX
XX Synthetic polypeptide(s) contg. specified heptad units - expressed in
PT vivo in plants to serve as custom-tailored storage proteins with
PT specified aminoacid content.
XX
XX Claim 7; Page 102; 176pp; English.
XX
CC The sequence represents a synthetic polypeptide comprising heptad units
CC of the peptide. The synthetic polypeptide can be expressed in vivo in
CC plants to serve as a synthetic seed storage protein which can be custom-
CC tailored for specific end-user requirements. The DNA encoding the heptad
CC may be used to transform plants to increase the content of partic. amino
CC acids such as lysine or methionine in seeds or leaves. See also AAR31979-
CC
```

```
CC 86 and AAR32659-705. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWKNVHLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::|::|::|::|::|::|::|

RESULT 38
AAR78255
ID AAR78255 standard; peptide; 28 AA.
XX
AC AAR78255;
XX
XX 15-JUL-1996 (first entry)
XX
XX SSP(5) 4 heptad.
XX
XX Lysine; synthetic storage protein; SSP; Vector; pSK6;
XX dihydrodipicolinic acid synthase; corn; maize; Zea mays; soybean;
XX Glycine max; transgenic plant; essential amino acid.
XX
XX Synthetic.
XX
XX WO9515392-A1.
XX
XX PD 08-JUN-1995.
XX
XX PF 21-NOV-1994; 94WO-US013190.
XX
XX PR 30-NOV-1993; 93US-00160117.
XX
XX PR 17-JUN-1994; 94US-00261661.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, Keeler SJ, Rice JA;
XX
XX WPI; 1995-215272/28.
XX
XX N-PSDB; AAQ94998.
XX
XX New chimeric gene providing increased lysine content in plant seeds -
XX contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
XX transport sequence and seed specific promoter, also new plants of
XX improved nutritional value.
XX
XX Example 8; Page 81; 180pp; English.
XX
XX Oligonucleotide SM96 (AAQ94998) and complementary sequence SM97
XX (AAQ94999) code for 4 repeats (AAR78255) of heptad peptide SSP5 (see also
XX AAR78238). Clone 3-5 (AAQ95006) was obt'd. by insertion of the first 22
XX bases of the SM96-SM97 set into the EarI site of clone 82-4 (see
XX AAQ94992) and transformation of Escherichia coli DHS alpha. Synthetic
XX storage protein SSP3-5 (AAR78260) encoded by the construct was used to
XX raise the lysine content in seeds of transformed tobacco, soybean and
XX corn
XX
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
QY 1 KIRALKWKNVHLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28
|::|::|::|::|::|::|::|::|

RESULT 39
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AAR78250
ID AAR78250 standard; protein; 28 AA.
XX
AC AAR78250;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .7
FT Peptide /label= SSP5
FT Peptide 8. .14
FT Peptide /label= SSP5
FT Peptide 15. .21
FT Peptide /label= SSP5
FT Peptide 22. .28
FT Peptide /label= SSP5
XX
FN W09515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
XX
DR N-PSDB; AAQ94993.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 136; 180pp; English.
XX
CC Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78250) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obtd. by insertion of HPLC-purified SSP5
CC -encoding oligonucleotides (AAQ94974-75) into pSK6 and use of the
CC resulting vector to transform Escherichia coli JM103, yielding clone 84-
CC H3 (AAQ94993). The SSP forms a coiled-coil structure. It can be expressed
CC in the seeds of transformed plants, e.g. soybean and corn, to increase
CC lysine content
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

OY 1 KIRALKWKNKHLKQBIKIALEQEIQA 25
DB 4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28

RESULT 40
AAR78244
ID AAR78244 standard; protein; 28 AA.
XX
AC AAR78244;

```

```

XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX
KW Lysine; synthetic storage protein; SSP; vector; pSK6;
KW dihydrodipicolinic acid synthase; corn; maize; soybean;
KW Glycine max; transgenic plant; essential amino acid.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .7
FT Peptide /label= SSP5
FT Peptide 8. .14
FT Peptide /label= SSP5
FT Peptide 15. .21
FT Peptide /label= SSP5
FT Peptide 22. .28
FT Peptide /label= SSP5
XX
FN W09515392-A1.
XX
PD 08-JUN-1995.
XX
PF 21-NOV-1994; 94WO-US013190.
XX
PR 30-NOV-1993; 93US-00160117.
PR 17-JUN-1994; 94US-00261661.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Falco SC, Keeler SJ, Rice JA;
XX
DR WPI; 1995-215272/28.
XX
DR N-PSDB; AAQ94983.
XX
PT New chimeric gene providing increased lysine content in plant seeds -
PT contains di:hydro:di:picolinic acid synthase gene coupled to chloroplast
PT transport sequence and seed specific promoter, also new plants of
PT improved nutritional value.
XX
PS Example 8; Page 129; 180pp; English.
XX
CC Lysine-rich synthetic storage protein Ssp 5.5.5.5 (AAR78244) comprises 2
CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
CC derived from vector pSK6. It was obtd. by insertion of SSP5-encoding
CC oligonucleotides (AAQ94974-75) into pSK6 and use of the resulting vector
CC to transform Escherichia coli JM103, yielding clone D33 (AAQ94983). The
CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
CC transformed plants, e.g. soybean and corn, to increase lysine content
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

OY 1 KIRALKWKNKHLKQBIKIALEQEIQA 25
DB 4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28

RESULT 41
AAR78242
ID AAR78242 standard; protein; 28 AA.
XX
AC AAR78242;
XX
DT 15-JUL-1996 (first entry)
XX
DE SSP 5.5.5.5.
XX

```

KW Lysine; synthetic storage protein; SSP; vector; PSK6;
 KW dihydrodipicolinic acid synthase; corn; maize; zea mays; soybean;
 KW Glycine max; transgenic plant; essential amino acid.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..7 /label= SSP5

FT Peptide 8..14 /label= SSP5

FT Peptide 15..21 /label= SSP5

FT Peptide 22..28 /label= SSP5

FT Peptide /label= SSP5

XX WO9515392-A1.

XX 08-JUN-1995.

XX 21-NOV-1994; 94WO-US013190.

XX 30-NOV-1993; 93US-00160117.

XX 17-JUN-1994; 94US-00261661.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Falco SC, Keeler SJ, Rice JA;

XX WPI; 1995-215272/28.

XX N-PSDB; AAQ94981.

XX New chimeric gene providing increased lysine content in plant seeds -
 PT contains dihydrodipicolinic acid synthase gene coupled to chloroplast
 PT transport sequence and seed specific promoter, also new plants of
 PT improved nutritional value.

XX Example 8; Page 127; 180pp; English.

XX Lysine-rich synthetic storage protein SSP 5.5.5.5 (AAR78242) comprises 2
 CC heptad SSP5 repeats (see AAR78238) flanked by SSP5 heptads (see AAR78236)
 CC derived from vector PSK6. It was obtd. by insertion of SSP5-encoding
 CC oligonucleotides (AAQ94974-75) into PSK6 and use of the resulting vector
 CC to transform Escherichia coli JM103, yielding clone D16 (AAQ94981). The
 CC SSP forms a coiled-coil structure. It can be expressed in the seeds of
 CC transformed plants, e.g. soybean and corn, to increase lysine content

XX Sequence 28 AA;

Query Match 26.3%; Score 36; DB 2; Length 28;

Best Local Similarity 24.0%; Pred. No. 1.1e+03;

Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAAALQETAA 25

DB 4 KMKAMEEKMKAMEEKMKAMEEKMA 28

RESULT 42

AAW62935

ID AAW62935 standard; peptide; 28 AA.

XX AC AAW62935;

XX 02-OCT-1998 (first entry)

XX Minimalist lytic peptide.

XX Lytic peptide; channel forming peptide; antibacterial; amphipathic.

XX Synthetic.

XX US5789542-A.

XX 04-AUG-1998.
 XX 06-OCT-1997; 97US-00944133.
 XX 22-APR-1994; 94US-00232525.
 XX 22-JUL-1996; 96US-00681075.
 XX 03-FEB-1997; 97US-00789077.
 XX (LOUJ) UNIV LOUISIANA STATE & AGRIC & MECH COLL.

XX Becker CL, McLaughlin ML;

XX WPI; 1998-446183/38.

XX Selective lysis of bacteria amongst mammalian cells - using 14-mer or 21-
 PT mer lytic peptides.

XX Disclosure; Col 5; 25pp; English.

XX AAW62920-67 represent minimalist lytic (channel forming) peptides. The
 CC peptides have antibacterial properties in concentrations not lethal
 CC toward mammalian cells. The peptides are heptads (or heptad multimers)
 CC that comprise four nonpolar amino acid residues and three positively
 CC charged amino acid residues, or five nonpolar amino acid residues and two
 CC positively charged amino acid residues. The nonpolar amino acid residues
 CC and the positively charged amino acid residues are distributed within the
 CC heptad such that when the multimer forms an alpha-helix the nonpolar
 CC amino acid residues will lie on one face of the alpha-helix, and the
 CC positively charged amino acid residues will lie on the opposite face of
 CC the alpha -helix, whereby the multimer is amphipathic

XX Sequence 28 AA;

Query Match 26.3%; Score 36; DB 2; Length 28;

Best Local Similarity 34.6%; Pred. No. 1.1e+03;

Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 IRALKWNAHLKQETAAALQETAALE 27

DB 3 LRALKKALKALKALKALKALKALK 28

RESULT 43

AAW60508

ID AAW60508 standard; protein; 28 AA.

XX AC AAW60508;

XX 25-MAR-2003 (revised)

XX 25-AUG-1998 (first entry)

XX Synthetic storage protein of the specification.

XX Dihydrodipicolinic acid synthase; DHPS; chimeric gene; storage protein;
 KW lysine inhibition; plant chloroplast transit sequence;
 KW plant seed-specific regulatory sequence; transgenic plant;
 KW increased lysine level; corn; Zea mays; soybean; Glycine max.

XX Synthetic.

XX US5773691-A.

XX 30-JUN-1998.

XX 07-JUN-1995; 95US-00474633.

XX 19-MAR-1992; 92US-00855414.

XX 18-MAR-1993; 93WO-US002480.

XX 06-JAN-1994; 94US-00178212.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Falco SC;
 XX WPI; 1998-387117/33.
 XX Chimeric genes encoding lysine production enzymes - useful for increasing
 XX transgenic seed lysine content without being inhibited by high levels of
 XX the amino acid.
 XX Example 21; Col 113-114; 106pp; English.
 XX The present sequence represents a synthetic lysine rich, storage protein
 XX of the specification. The sequence can be operably linked to a seed-
 XX specific regulatory sequence to create a chimeric gene of the
 XX specification. The specification also describes a *Corynebacterium* dapA
 XX gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme,
 XX which was used to create chimeric genes of the invention. The chimeric
 XX genes contain a nucleic acid fragment encoding a DHDPS enzyme which is
 XX insensitive to inhibition by lysine operably linked to a plant
 XX chloroplast transit sequence and to a plant seed-specific regulatory
 XX sequence. The chimeric genes are useful for producing plants containing
 XX increased levels of lysine, especially in corn (Zea mays) and soybean
 XX (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 28 AA;
 Query Match 26.3%; Score 36; DB 2; Length 28;
 Best Local Similarity 24.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KIRALKWNAHLKQFIAALQEQIAA 25
 |::||::| ::::|:::|
 Db 4 KKKAMEEKWKAMEEKWKAMEEKKA 28
 RESULT 44
 AAW60516
 ID AAW60516 standard; protein; 28 AA.
 XX AAW60516;
 XX 25-MAR-2003 (revised)
 DT 25-AUG-1998 (first entry)
 DE Synthetic storage protein of the specification.
 XX Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein;
 XX lysine inhibition; plant chloroplast transit sequence;
 XX plant seed-specific regulatory sequence; transgenic plant;
 XX increased lysine level; corn; Zea mays; soybean; Glycine max.
 XX Synthetic.
 OS US5773691-A.
 XX 30-JUN-1998.
 PD 07-JUN-1995; 95US-00474633.
 PF 19-MAR-1992; 92US-00855414.
 PR 18-MAR-1993; 93WO-US002480.
 PR 06-JAN-1994; 94US-00178212.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Falco SC;
 PI WPI; 1998-387117/33.
 DR N-PSDB; AAV35831.
 XX Chimeric genes encoding lysine production enzymes - useful for increasing
 XX transgenic seed lysine content without being inhibited by high levels of
 XX the amino acid.

PS Example 21; Col 125-136; 106pp; English.
 XX The present sequence represents a synthetic lysine rich, storage protein
 XX of the specification. The sequence can be operably linked to a seed-
 XX specific regulatory sequence to create a chimeric gene of the
 XX specification. The specification also describes a *Corynebacterium* dapA
 XX gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme,
 XX which was used to create chimeric genes of the invention. The chimeric
 XX genes contain a nucleic acid fragment encoding a DHDPS enzyme which is
 XX insensitive to inhibition by lysine operably linked to a plant
 XX chloroplast transit sequence and to a plant seed-specific regulatory
 XX sequence. The chimeric genes are useful for producing plants containing
 XX increased levels of lysine, especially in corn (Zea mays) and soybean
 XX (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 28 AA;
 Query Match 26.3%; Score 36; DB 2; Length 28;
 Best Local Similarity 24.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 KIRALKWNAHLKQFIAALQEQIAA 25
 |::||::| ::::|:::|
 Db 4 KKKAMEEKWKAMEEKWKAMEEKKA 28
 RESULT 45
 AAW60510
 ID AAW60510 standard; protein; 28 AA.
 XX AAW60510;
 XX 25-MAR-2003 (revised)
 DT 25-AUG-1998 (first entry)
 DE Synthetic storage protein of the specification.
 XX Dihydrodipicolinic acid synthase; DHDPS; chimeric gene; storage protein;
 XX lysine inhibition; plant chloroplast transit sequence;
 XX plant seed-specific regulatory sequence; transgenic plant;
 XX increased lysine level; corn; Zea mays; soybean; Glycine max.
 XX Synthetic.
 OS US5773691-A.
 XX 30-JUN-1998.
 PD 07-JUN-1995; 95US-00474633.
 PF 19-MAR-1992; 92US-00855414.
 PR 18-MAR-1993; 93WO-US002480.
 PR 06-JAN-1994; 94US-00178212.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Falco SC;
 PI WPI; 1998-387117/33.
 DR Chimeric genes encoding lysine production enzymes - useful for increasing
 XX transgenic seed lysine content without being inhibited by high levels of
 XX the amino acid.
 XX Example 21; Col 115-116; 106pp; English.
 XX The present sequence represents a synthetic lysine rich, storage protein
 XX of the specification. The sequence can be operably linked to a seed-
 XX specific regulatory sequence to create a chimeric gene of the
 XX specification. The specification also describes a *Corynebacterium* dapA
 XX gene, which encodes a dihydrodipicolinic acid synthase (DHDPS) enzyme,
 XX which was used to create chimeric genes of the invention. The chimeric
 XX genes contain a nucleic acid fragment encoding a DHDPS enzyme which is

```

CC insensitive to inhibition by lysine operably linked to a plant
CC chloroplast transit sequence and to a plant seed-specific regulatory
CC sequence. The chimeric genes are useful for producing plants containing
CC increased levels of lysine, especially in corn (Zea mays) and soybean
CC (Glycine max). (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 28 AA;
Query Match 26.3%; Score 36; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
Qy 1 KIRALKWNAHLKOEIAALAEQEIAA 25
| : | : | : : : : | : : : : |
Db 4 KMKAMEEKMKAMEEKKMKAMEEKMA 28
Search completed: November 21, 2005, 21:40:24
Job time : 131 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:36:04 ; Search time 23.5 Seconds
(without alignments)

114.641 Million cell updates/sec

Title: US-10-088-417a-4

Perfect score: 137

Sequence: 1 KIRALKWNAHLKQETAALEQETAALEQ 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 199

Minimum DB seq length: 28

Maximum DB seq length: 28

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	16.8	28	2	similarity to yeas
2	23	16.8	28	2	hypothetical prote
3	22	16.1	28	2	RAS protein [impor
4	21	15.3	28	2	ribosomal protein
5	21	15.3	28	2	brevicin-27 - Lact
6	21	15.3	28	2	gene LFY protein -
7	21	15.3	28	2	cell surface prote
8	20	14.6	28	2	lysosomal acid lip
9	20	14.6	28	2	hypothetical prote
10	20	14.6	28	2	nicotinic acetylch
11	20	14.6	28	2	hypothetical prote
12	19.5	14.2	28	2	ribosomal protein
13	19	13.9	28	2	antigen, T-cell re
14	19	13.9	28	2	aryl acylamidase -
15	19	13.9	28	2	homeobox JRX prote
16	19	13.9	28	4	frame shifted FMR1
17	18	13.1	28	2	bombyxin-IV chain
18	18	13.1	28	2	omega-glialdin - ei
19	18	13.1	28	2	stp protein (Baker
20	18	13.1	28	2	hypothetical prote
21	18	13.1	28	2	ZF3 domain - human
22	18	13.1	28	2	hypothetical prote
23	18	13.1	28	2	peroxisome prolife
24	18	13.1	28	2	peroxisome prolife
25	17.5	12.8	28	2	cellular retinol-b
26	17	12.4	28	1	trp operon leader
27	17	12.4	28	2	NADH2 dehydrogenas
28	17	12.4	28	2	glutathione transf
29	17	12.4	28	2	rRNA N-glycosidase

30	16	11.7	28	1	G9BPSV
31	16	11.7	28	2	A38296
32	16	11.7	28	2	A60291
33	16	11.7	28	2	A32643
34	16	11.7	28	2	A61322
35	16	11.7	28	2	S21231
36	16	11.7	28	2	I45911
37	16	11.7	28	2	B54127
38	16	11.7	28	2	T06340
39	15	10.9	28	2	S66436
40	15	10.9	28	2	D38578
41	15	10.9	28	2	A35115
42	15	10.9	28	2	S07156
43	15	10.9	28	2	A27261
44	15	10.9	28	2	PL0005
45	15	10.9	28	2	PC2239

ALIGNMENTS

RESULT 1

T38041

similarity to yeast mating protein SSF1 - fission yeast (Schizosaccharomyces pombe) (fra
C;Species: Schizosaccharomyces pombe
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
C;Accession: T38041
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21764
A;Accession: T38041
A;Status: preliminary; translated from GE/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-28 <MCD>
A;Cross-references: UNIPARC:UPI0000162058; EMBL:AL109951; PIDN:CAB53054.1; GSPDB:GN00066
A;Experimental source: strain 972h-; cosmid c1B9
C;Genetics:
A;Gene: SPDB:SPAC1B9.01c
A;Map position: 1

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	8	KNAHLKQS	15
Db	11	KRTHLKAD	18

RESULT 2

H85908

hypothetical protein Z3917 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85908
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <STO>
A;Cross-references: UNIPROT:Q8X415; UNIPARC:UPI00000D0867; GB:AE005174; NID:G12517049; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3917

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 18 ALRQEIADLE 27
| | | : | |
Db 18 ATBEETSLLE 27

RESULT 3
T47196
RAS protein [imported] - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47196
R;Lee, C.W.; Lee, E.
A:Submitted to the EMBL Data Library, August 1995
A:Description: Structural analysis of ras genes from filamentous fungi.
A:Reference number: Z24384
A:Accession: T47196
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-28 <LEE>
A:Cross-references: UNIPROT:P22126; UNIPARC:UPI000016891F; EMBL:U33746; FIDN:AAA74986.1
C:Genetics:
A:Gene: ras
C:Note: Intron positions not resolved (incomplete sequence)
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 9 NAHLKQEIADLEQEIADLE 27
| | | : | | : | |
Db 1 DSYRKQ--CTIDNEVALLD 17

RESULT 4
S51067
ribosomal protein S16 - Thermus aquaticus (fragment)
C:Species: Thermus aquaticus
C:Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
C:Accession: S51067
R;Tsiboli, P.; Herfurth, E.; Choli, T.
Eur. J. Biochem. 226, 169-177, 1994
A:Title: Purification and characterization of the 30S ribosomal proteins from the bacterium Thermus aquaticus
A:Reference number: S51053; MUID:95045586; PMID:7957245
A:Accession: S51067
A:Molecule type: protein
A:Residues: 1-28 <TSI>
A:Cross-references: UNIPARC:UPI00001772B2
A:Note: the source is designated as Thermus thermophilus
C:Superfamily: Escherichia coli ribosomal protein S16
C:Keywords: protein biosynthesis; ribosome

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.7e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 KIRALKWKNAH 11
| | | : | |
Db 3 KIRLAREGSKH 13

RESULT 5
A56499
brevicin-27 - Lactobacillus brevis (strain SB27) (fragment)
C:Species: Lactobacillus brevis
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: A56499
R;Benoit, V.; Lebrini, A.; Humbert, G.; Lefebvre, G.
submitted to the Protein Sequence Database, June 1995
A:Description: Partial amino acid sequence of brevicin27, a bacteriocin which shares no similarity with other known bacteriocins
A:Reference number: A56499
A:Accession: A56499
A>Status: preliminary

A:Molecule type: protein
A:Residues: 1-28 <LEB>
A:Cross-references: UNIPARC:UPI000017AD13

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ALKWKNA 10
| | | : | |
Db 8 AXTWGNA 14

RESULT 6
T09594
gene LFY protein - Monterey pine (fragment)
C:Species: Pinus radiata (Monterey pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09594
R;Izquierdo, L.X.; Vergara, R.F.; Alvarez-Buylla, E.R.
submitted to the EMBL Data Library, August 1996
A:Description: Partial characterization of Pinus radiata meristem identity homolog gene
A:Reference number: Z16756
A:Accession: T09594
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-28 <IZQ>
A:Cross-references: UNIPROT:O24285; UNIPARC:UPI00000AC880; EMBL:U66725; NID:g1513305; PII:1513305
C:Genetics:
A:Gene: LFY
C:Function:
A:Description: controls meristem identity

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 22.2%; Pred. No. 1.7e+04;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KIRALKWKNN 9
| | | : | |
Db 19 RLKGRAWN 27

RESULT 7
A44877
cell surface protein 2F5 91K component - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44877
R;Nardi, J.B.
Dev. Biol. 152, 161-171, 1992
A:Title: Dynamic expression of a cell surface protein during rearrangement of epithelial cells
A:Reference number: A44877; MUID:92331807; PMID:1628754
A:Accession: A44877
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-28 <NAR>
A:Cross-references: UNIPROT:Q9TWX0; UNIPARC:UPI000007FF81
A:Note: sequence extracted from NCBI backbone (NCBIP:108784)

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 1.7e+04;
Matches 5; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 7 WKNA----HLKQEIADLE 20
| | | : | | : | |
Db 5 WRVADSLSEVKQIESFE 22

RESULT 8
I55596
lysosomal acid lipase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C;Accession: I55596
 R;Klima, H.; Ullrich, K.; Aelaniadis, C.; Fehring, P.; Lackner, K.J.; Schmitz, G.
 J. Clin. Invest. 92, 2713-2718, 1993
 A;Title: A splice junction mutation causes deletion of a 72-base exon from the mRNA for
 A;Reference number: I55596; MUID:94075617; PMID:8254026
 A;Accession: I55596
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-28 <RES>
 A;Cross-references: UNIPARC:UPI000011F7AC; GB:S68069; NID:G544574; PIDN:AAB29185.1; PID:
 C;Superfamily: triacylglycerol lipase, lingual

Query Match 14.6%; Score 20; DB 2; Length 28;
 Best Local Similarity 42.9%; Pred. No. 2.3e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKW 7
 Db 21 KFOAFDW 27

RESULT 9

S15235
 hypothetical protein - Pseudomonas aeruginosa
 C;Species: Pseudomonas aeruginosa
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 A;Accession: S15235
 R;Perry, A.C.F.; Bhriain, N.N.; Brown, N.L.; Rouch, D.A.
 Mol. Microbiol. 5, 163-171, 1991
 A;Title: Molecular characterization of the gor gene encoding glutathione reductase from
 ses.
 A;Reference number: S15235; MUID:91194546; PMID:1849605
 A;Accession: S15235
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <PER>
 A;Cross-references: UNIPROT:P23205; UNIPARC:UPI000016FCAP; EMBL:X54201; NID:G45324; PIDN:

Query Match 14.6%; Score 20; DB 2; Length 28;
 Best Local Similarity 35.3%; Pred. No. 2.3e+04;
 Matches 6; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 11 HLKQEIQALEDIAALE 27
 Db 7 HLALHPDLDCIAPYE 23

RESULT 10

S68643
 nicotinic acetylcholine receptor-binding protein 3C - black-banded coral snake (fragment)
 C;Species: Micrurus nigrocinctus (black-banded coral snake)
 C;Date: 23-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 A;Accession: S68643
 R;Alape-Giron, A.; Stiles, B.; Schmidt, J.; Giron-Cortes, M.; Thelestam, M.; Joernvall,
 FEBS Lett. 380, 29-32, 1996
 A;Title: Characterization of multiple nicotinic acetylcholine receptor-binding proteins
 A;Reference number: S68639; MUID:96181662; PMID:8603741
 A;Accession: S68643
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-28 <ALA>

Query Match 14.6%; Score 20; DB 2; Length 28;
 Best Local Similarity 57.1%; Pred. No. 2.3e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KIRALKW 7
 Db 22 KIXPKKW 28

RESULT 11

C83969
 hypothetical protein BH2555 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 A;Accession: C83969
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: C83969
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <STO>
 A;Cross-references: UNIPROT:Q9K9U0; UNIPARC:UPI000000C3F36; GB:AF001515; GB:BA0000004; NID:
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH2555

Query Match 14.6%; Score 20; DB 2; Length 28;
 Best Local Similarity 30.0%; Pred. No. 2.3e+04;
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQE 15
 Db 12 KLMRVHISQ 21

RESULT 12

S72460
 ribosomal protein S19 - curled-leaved tobacco chloroplast (fragment)
 C;Species: Chloroplast Nicotiana glauca (curled-leaved tobacco)
 C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 A;Accession: S72460
 R;Goulding, S.B.; Olmstead, R.G.; Morden, C.W.; Wolfe, K.H.
 Mol. Gen. Genet. 252, 195-206, 1996
 A;Title: Ebb and flow of the chloroplast inverted repeat.
 A;Reference number: S72459; MUID:96397499; PMID:8804393
 A;Accession: S72460
 A;Status: translation not shown

A;Molecule type: DNA
 A;Residues: 1-28 <GOU>
 A;Cross-references: UNIPROT:Q36593; UNIPARC:UPI000008D033; EMBL:Z71241; NID:G1279593; PI
 A;Note: only a part of the nucleic acid sequence is shown
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1996
 C;Genetics:
 A;Gene: rps19
 A;Genome: chloroplast
 A;Start codon: GTG
 C;Function:

A;Pathway: protein biosynthesis
 C;Superfamily: ribosomal protein S19/S15
 C;Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 14.2%; Score 19.5; DB 2; Length 28;
 Best Local Similarity 42.9%; Pred. No. 2.6e+04;
 Matches 9; Conservative 3; Mismatches 4; Indels 5; Gaps 2;

Qy 3 RALKWQNA----HLKQEIALL 19
 Db 3 RSLK-KNPFVANHLKKIDKL 22

RESULT 13

I59477
 antigen, T-cell receptor - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
 A;Accession: I59477
 R;Mathioudakis, G.; Chen, P.
 Scand. J. Immunol. 38, 31-36, 1993
 A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the
 T cell donors.
 A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-28 <RES>
A;Cross-references: UNIPARC:UPI0000117281; GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:
C;Keywords: T-cell receptor

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 WKNAHLKQ 14
| | | | |
Db 4 WDPATYKK 11
| | | | |

RESULT 14
S16228
aryl acylamidase - Nocardia globerulea
C;Species: Nocardia globerulea
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S16228
R;Yoshioka, H.; Nagasawa, T.; Yamada, H.
Eur. J. Biochem. 199, 17-24, 1991
A;Title: Purification and characterization of aryl acylamidase from Nocardia globerulea.
A;Reference number: S16228; MUID:91293120; PMID:2065673
A;Accession: S16228
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <EUR>
A;Cross-references: UNIPROT:P80008; UNIPARC:UPI00001260D8

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 35.0%; Pred. No. 3.1e+04;
Matches 7; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 10 AHLKQBIAAI--RQETAALE 27
| | | | |
Db 8 AHDTGLAEILREGQVSACE 27
| | | | |

RESULT 15
PN0625
homeobox JRX protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 05-Oct-2004
C;Accession: PN0625
R;Inamori, K.; Takeshita, K.; Chiba, S.; Yazaki, Y.; Hirai, H.
Biochem. Biophys. Res. Commun. 195, 203-208, 1993
A;Title: Identification of homeobox genes expressed in human T-lymphocytes.
A;Reference number: PN0625; MUID:94029995; PMID:8105782
A;Accession: PN0625
A;Molecule type: DNA
A;Residues: 1-28 <INA>
A;Cross-references: UNIPROT:Q9UD92; UNIPARC:UPI000006F5FA
A;Experimental source: T-lymphocyte
C;Comment: This protein is the product of the divergent classes of homeobox gene and par
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 13.9%; Score 19; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 3.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KQBIAA 18
| | | | |
Db 12 KAEIAA 17
| | | | |

RESULT 16
I68614
frame shifted FMR1 exon - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: I68614; I68615
R;Eichler, E.E.; Richards, S.; Gibbs, R.A.; Nelson, D.L.
Hum. Mol. Genet. 2, 1147-1153, 1993
A;Title: Fine structure of the human FMR1 gene.
A;Reference number: I54334; MUID:94004853; PMID:8401496
A;Accession: I68614
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <EII>
A;Cross-references: UNIPROT:Q16578; UNIPARC:UPI000006DBIC; GB:L19490; NID:g388747; PIDN:
A;Accession: I68615
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-28 <EII2>
A;Cross-references: UNIPARC:UPI000006DBIC; GB:L19491; NID:g388749; PIDN:AAA62467.1; PID:
C;Comment: This sequence appears to be the frame shifted hypothetical translation of an e
C;Genetics:
A;Gene: GDB:FMR1
A;Cross-references: GDB:129038; OMIM:309550
A;Map position: Xq27.3-Xq27.3

Query Match 13.9%; Score 19; DB 4; Length 28;
Best Local Similarity 37.5%; Pred. No. 3.1e+04;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 11 HLKQETAALEQETIAAL 26
| | | | |
Db 12 HVIQERLKEEQRTCL 27
| | | | |

RESULT 17
JT0412
bombyxin-IV chain B - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
C;Accession: JT0412
R;Maruyama, K.; Hietter, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki,
Agric. Biol. Chem. 52, 3035-3041, 1988
A;Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bon
A;Reference number: JT0410
A;Accession: JT0412
A;Molecule type: protein
A;Residues: 1-28 <MAR>
A;Cross-references: UNIPARC:UPI000017665E
C;Superfamily: insulin
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Disulfide bonds: interchain (to chain A-7) #status predicted
F;22/Disulfide bonds: interchain (to chain A-20) #status predicted

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 4.1e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 HLKQETIAAL 19
| | | | |
Db 13 HLANTLADL 21
| | | | |

RESULT 18
A03356
omega-gliadin - einkorn wheat (fragment)
C;Species: Triticum monococcum (einkorn wheat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A03356
R;Shewry, P.R.; Autran, J.C.; Nimmo, C.C.; Lew, E.J.L.; Kasarda, D.D.
Nature 286, 520-522, 1980
A;Reference number: A93228
A;Accession: A03356
A;Molecule type: protein
A;Residues: 1-28 <SHE>
A;Cross-references: UNIPROT:P02865; UNIPARC:UPI000012B3AA
C;Superfamily: gliadin

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 33.3%; Pred. No. 4.1e+04;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 20 EQEIAALEQ 28
 :||:|:
 Db 8 DQELQSPQQ 16

RESULT 19
 S49924
 stp protein (Baker variant) - phage OX2
 C;Species: phage OX2
 C;Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S55803; S49924
 R;Penner, M.; Morad, I.; Snyder, L.; Kaufmann, G.
 J. Mol. Biol. 249, 857-868, 1995
 A;Title: Phage T4-coded Stp: double-edged effector of coupled DNA and tRNA-restriction
 A;Reference number: S55796; MUID:95311310; PMID:7791212
 A;Accession: S55803
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-28 <PEN>
 A;Cross-references: UNIPROT:Q38060; UNIPARC:UPI000009C058; EMBL:Z46880; NID:G599663; PID
 C;Genetics:
 A;Gene: stp
 C;Superfamily: phage T4 stp protein

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 50.0%; Pred. No. 4.1e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 NAHLKQ 14
 :||:
 Db 6 NEHVMQ 11

RESULT 20
 S64701
 hypothetical protein (aph1 5'-region) - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C;Accession: S64701
 R;Huang, Y.; Garrison, P.N.; Barnes, L.D.
 Biochem. J. 312, 925-932, 1995
 A;Title: Cloning of the Schizosaccharomyces pombe gene encoding diadenosine 5',5'-P(1)
 n family.
 A;Reference number: S64700; MUID:96128081; PMID:8554540
 A;Accession: S64701
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <HUA>
 A;Cross-references: UNIPARC:UPI000017B1D8; EMBL:U32615

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 23.1%; Pred. No. 4.1e+04;
 Matches 3; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 8 KNAHLKQEIAALE 20
 :||:|:
 Db 14 REAEFNQQLRFLQ 26

RESULT 21
 I39288
 ZF3 domain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C;Accession: I39288
 R;Ogawa, O.; Eccles, M.R.; Yun, K.; Mueller, R.F.; Holdaway, M.D.; Reeve, A.E.
 Hum Mol Genet. 2, 203-204, 1993
 A;Title: A novel insertional mutation at the third zinc finger coding region of the WT1

A;Reference number: I39288; MUID:93271969; PMID:8098976
 A;Accession: I39288
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-28 <RES>
 A;Cross-references: UNIPARC:UPI00000006BE; EMBL:X72314; NID:G312849; PIDN:CAA51057.1; PFI
 C;Genetics:
 A;Gene: GDB:WT1
 A;Cross-references: GDB:120496; OMIM:194070
 A;Map position: 11p13-11p13

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 50.0%; Pred. No. 4.1e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KNAHLK 13
 :||:
 Db 11 RSDHLK 16

RESULT 22
 S70894
 hypothetical protein 1 - Vibrio anguillarum (fragment)
 C;Species: Vibrio anguillarum
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S70894
 R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
 Mol. Microbiol. 19, 625-637, 1996
 A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen
 A;Reference number: S70894; MUID:96228710; PMID:8830252
 A;Accession: S70894
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <OTO>
 A;Cross-references: UNIPROT:Q9ZB83; UNIPARC:UPI000000BD25A; GB:U36378; EMBL:L47344; NID:G

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 33.3%; Pred. No. 4.1e+04;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KWKNAH 11
 :||:
 Db 10 EWQVTH 15

RESULT 23
 PC4430
 peroxisome proliferator activated receptor gamma variant, P12A - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
 C;Accession: PC4430
 R;Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K.
 Biochem. Biophys. Res. Commun. 241, 270-274, 1997
 A;Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
 A;Reference number: PC4429; MUID:98086341; PMID:9425261
 A;Accession: PC4430
 A;Molecule type: DNA
 A;Residues: 1-28 <YEN>
 A;Cross-references: UNIPARC:UPI000017ALD0
 C;Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
 C;Genetics:
 A;Introns: 28/1

Query Match 13.1%; Score 18; DB 2; Length 28;
 Best Local Similarity 42.9%; Pred. No. 4.1e+04;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 NAHLKQE 15
 :||:|:
 Db 22 SANISQE 28

RESULT 24

PC4429
peroxisome proliferator activated receptor gamma - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: PC4429
R:Yen, C.J.; Beamer, B.A.; Negri, C.; Silver, K.; Brown, K.A.; Yarnall, D.P.; Burns, D.K.
Biochem. Biophys. Res. Commun. 241, 270-274, 1997
A:Title: Molecular scanning of the human peroxisome proliferator activated receptor gamma
A:Reference number: PC4429; MUID:98086341; PMID:9425261
A:Accession: PC4429
A:Molecule type: DNA
A:Residues: 1-28 <YEN>
A:Cross-references: UNIPARC:UPI000017A1CF
C:Comment: This nuclear receptor protein regulates adipocyte differentiation, lipid and
C:Genetics:
A:Introns: 28/1

Query Match 13.1%; Score 18; DB 2; Length 28;
Best Local Similarity 42.3%; Pred. No. 4.1e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 NAHLKQE 15
|:|:|:
DB 22 SANISQE 28

RESULT 25
A61113
cellular retinol-binding protein II - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A61113
R:Finlay, J.A.; DeLuca, H.F.
Biochemistry 27, 3381-3387, 1988
A:Title: Purification and properties of an 18-kilodalton, 1,25-dihydroxyvitamin D-3 modu
A:Reference number: A61113; MUID:88269534; PMID:3390438
A:Accession: A61113
A:Molecule type: protein
A:Residues: 1-28 <FIN>
A:Cross-references: UNIPROT:Q7LZ76; UNIPARC:UPI0000177825
C:Superfamily: myelin P2 protein

Query Match 12.8%; Score 17.5; DB 2; Length 28;
Best Local Similarity 23.8%; Pred. No. 4.7e+04;
Matches 5; Conservative 6; Mismatches 7; Indels 3; Gaps 1;

QY 7 WK---NAHLKQEIAALEQEIFA 24
|:|:|:|:|:|:
DB 8 WEMESNPEGYNVALDIDFA 28

RESULT 26
LFSEW
trp operon leader peptide - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C:Accession: A03591
R:Miozzari, G.F.; Yanofsky, C.
Nature 276, 684-689, 1978
A:Title: The regulatory region of the trp operon of Serratia marcescens.
A:Reference number: A93202; MUID:79033989; PMID:366432
A:Accession: A03591
A:Molecule type: DNA
A:Residues: 1-28 <MIO>
A:Cross-references: UNIPROT:P03055; UNIPARC:UPI000012E89F
C:Genetics:
A:Gene: trpL
C:Function:
A:Description: Involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match 12.4%; Score 17; DB 1; Length 28;
Best Local Similarity 28.6%; Pred. No. 5.4e+04;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 WKNAHLK 13
|:|:|:
DB 20 WRTSLLR 26

RESULT 27
T14210
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Uromastix acanthinurus mitochondr
C:Species: mitochondrion Uromastix acanthinurus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T14210
R:Wacey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826; PMID:9000757
A:Accession: T14210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <MAC>
A:Cross-references: UNIPROT:P92760; UNIPARC:UPI0000099123; EMBL:U71325; NID:g1753264; PII
A:Experimental source: specimen voucher MVZ162567; Museum of Vertebrate Zoology, Universi
C:Genetics:
A:Genome: mitochondrion
A:Note: NDI
C:Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match 12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 44.4%; Pred. No. 5.4e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 HLKQEIAAL 19
|:|:|:
DB 15 NLPSALAAAL 23

RESULT 28
S21278
glutathione transferase (EC 2.5.1.18) alpha-Yx - rat (fragment)
N:Alternate names: glutathione S-transferase Yx; glutathione transferase Yfetus
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C:Accession: S21278
R:Igarashi, T.; Tsuchiya, T.; Shikata, Y.; Sagami, F.; Tagaya, O.; Horie, T.; Satoh, T.
Biochem. J. 283, 307-311, 1992
A:Title: Developmental aspects of a unique glutathione S-transferase subunit Yx in the l
Yfetus.
A:Reference number: S21278; MUID:92231842; PMID:1567376
A:Accession: S21278
A:Molecule type: protein
A:Residues: 1-28 <IGA>
A:Cross-references: UNIPROT:Q9JLQ6; UNIPARC:UPI00000E725F
C:Superfamily: glutathione transferase
C:Keywords: dimer; liver; transferase

Query Match 12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 14.3%; Pred. No. 5.4e+04;
Matches 1; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIRALKW 7
|:|:|:
DB 14 RMEPIRW 20

RESULT 29
S38524
rRNA N-glycosidase (EC 3.2.2.22) saporin R1 - common soapwort (fragment)
C:Species: Saponaria officinalis (common soapwort)
C:Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S38524
R:Ferreras, J.M.; Barbieri, L.; Girbes, T.; Battelli, M.G.; Rojo, M.A.; Arias, F.J.; Ro


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Biochim. Biophys. Acta 1216, 31-42, 1993
A;Title: Distribution and properties of major ribosome-inactivating proteins (28 S rRNA
A;Reference number: S38521; MUID:94032486; PMID:8218413
A;Accession: S38524
A;Molecule type: protein
A;Residues: 1-28 <FER>
A;Cross-references: UNIPROT:Q7MLI8; UNIPARC:UPI000017AF39
C;Keywords: glycosidase; hydrolase

Query Match      12.4%; Score 17; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 5.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      5 LKW 7
      :||
Db      4 VKW 6

RESULT 30
G9BRSV
Gene 9 protein - spiroplasma virus 4
C;Species: Spiroplasma virus 4, SpV4
A;Note: host Spiroplasma melliferum
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: B29825
R;Renaudin, J.; Pascarel, M.C.; Bove, J.M.
J. Bacteriol. 169, 4950-4961, 1987
A;Title: Spiroplasma virus 4: nucleotide sequence of the viral DNA, regulatory signals,
A;Reference number: A91845; MUID:88032809; PMID:2822658
A;Accession: B29825
A;Molecule type: DNA
A;Residues: 1-28 <REN>
A;Cross-references: UNIPROT:P11341; UNIPARC:UPI000013863B; GB:M17988; MID:G334998
A;Note: This ORF is not annotated in GenBank entry SPVDNA
C;Comment: This virus is a procaryote DNA virus.
C;Genetics:
A;Gene: 9
A;Genetic code: SGC3
C;Superfamily: spiroplasma virus 4 gene 9 protein

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.1e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      6 KWKN 9
      :||
Db      19 RWFN 22

RESULT 31
A38296
sterol esterase (EC 3.1.1.13) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 14-Nov-1997
C;Accession: A38296
R;DiPersio, L.P.; Fontaine, R.N.; Hui, D.Y.
J. Biol. Chem. 265, 16801-16806, 1990
A;Title: Identification of the active site serine in pancreatic cholesterol esterase by
A;Reference number: A38296; MUID:91009095; PMID:2211595
A;Accession: A38296
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-28 <DIP>
A;Cross-references: UNIPARC:UPI0000175911
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein

Query Match      11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.1e+04;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      16 IAALEQETAA 25
      || : |||

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Db 2 IALVITNIAA 11

RESULT 32

A60291

24K proteinase (EC 3.4.-.-) - silkworm (fragment)

C;Species: Bombyx mori (silkworm)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 15-Oct-1999

C;Accession: A60291

R;Ikeda, M.; Sasaki, T.; Yamashita, O.

Insect Biochem. 20, 725-734, 1990

A;Title: Purification and characterization of proteases responsible for vitellin degradation

A;Reference number: A60291

A;Accession: A60291

A;Molecule type: protein

A;Residues: 1-28 <IRE>

A;Cross-references: UNIPARC:UPI0000175C3C

C;Comment: This enzyme degrades the nutritional yolk protein vitellin during embryogenesis

C;Superfamily: trypsin; trypsin homology

C;Keywords: egg yolk; hydrolase

Query Match 11.7%; Score 16; DB 2; Length 28;

Best Local Similarity 40.0%; Pred. No. 7.1e+04;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 17 AALEQEIAAL 26

Db 19 ASMXNIAAL 28

RESULT 33

A32643

deoxyribodipyrimidine photo-lyase (EC 4.1.99.3) - Methanobacterium thermoautotrophicum

N;Alternate names: photoreactivating enzyme

C;Species: Methanobacterium thermoautotrophicum

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Apr-1999

C;Accession: A32643

R;Kiener, A.; Husain, I.; Sancar, A.; Walsh, C.

J. Biol. Chem. 264, 13880-13887, 1989

A;Title: Purification and properties of Methanobacterium thermoautotrophicum DNA photolyase

A;Reference number: A32643; MUID:89340481; PMID:2668276

A;Accession: A32643

A;Molecule type: protein

A;Residues: 1-28 <KIE>

A;Cross-references: UNIPARC:UPI00001319F6

C;Superfamily: deoxyribodipyrimidine photo-lyase

C;Keywords: carbon-carbon lyase; DNA binding

Query Match 11.7%; Score 16; DB 2; Length 28;

Best Local Similarity 60.0%; Pred. No. 7.1e+04;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIRAL 5

Db 6 RIRSL 10

RESULT 34

A61322

somatostatin-28 - sheep

N;Contains: somatostatin-14

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999

C;Accession: A61322; A61344

R;Spiess, J.; Villarreal, J.; Vale, W.

Biochemistry 20, 1982-1988, 1981

A;Title: Isolation and sequence analysis of a somatostatin-like polypeptide from ovine

A;Reference number: A61322; MUID:81184502; PMID:7225368

A;Accession: A61322

A;Molecule type: protein

A;Residues: 1-28 <SPI>

A;Cross-references: UNIPARC:UPI000002F1CD

R;Burgus, R.; Ling, N.; Butcher, M.; Guillemin, R.

Proc. Natl. Acad. Sci. U.S.A. 70, 684-688, 1973
A:Title: Primary structure of somatostatin, a hypothalamic peptide that inhibits the secretion of growth hormone releasing hormone
A:Reference number: A61344; MUID:73209562; PMID:4514982
A:Accession: A61344
A:Molecule type: protein
A:Residues: 15-28 <EUR>
A:Cross-references: UNIPARC:UPI000002BB13
C:Superfamily: somatostatin
C:Keywords: neuropeptide
F:1-28/Product: somatostatin-28 #status experimental <S28>
F:15-28/Product: somatostatin-14 #status experimental <S14>
F:17-28/Disulfide bonds: #status experimental

Query Match 11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WK 8
||
DB 22 WK 23

RESULT 35
S21231
calcium-binding protein SCP VI, sarcoplasmic - common lancelet
C:Species: Branchiostoma lanceolatum (common lancelet)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002
C:Accession: S21231
R:Tagaki, T.; Valette-Talbi, L.; Cox, J.A.
FEBS Lett. 302, 159-160, 1992
A:Title: Primary structure of three minor isoforms of amphioxus sarcoplasmic calcium-binding protein
A:Reference number: S21153; MUID:92339504; PMID:1633848
A:Accession: S21231
A:Molecule type: protein
A:Residues: 1-28 <TAK>
A:Cross-references: UNIPARC:UPI0000177710
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: calcium binding; EF hand

Query Match 11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 16.7%; Pred. No. 7.1e+04;
Matches 1; Conservative 4; Mismatches 1; Indels 1; Gaps 0;

QY 4 ALKWN 9
::: :
DB 14 SIQWMD 19

RESULT 36
I45911
dnaK-type molecular chaperone hsp70A - bovine (fragment)
N:Alternate names: heat shock protein
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
C:Accession: I45911
R:Kowalski, J.; Gilbert, S.A.; van Drunen-Littel-van den Hurk, J.; Bab
Vaccine 11, 1100-1107, 1993
A:Title: Heat-Shock Promoter-Driven Synthesis of Secreted Herpesvirus Glycoproteins in T
A:Reference number: I45911; MUID:94070117; PMID:8249428
A:Accession: I45911
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <KOW>
A:Cross-references: UNIPROT:Q27965; UNIPARC:UPI000016C320; GB:M98823; NID:g409185; PIDN:
C:Genetics:
A:Gene: hsp70A
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
C:Superfamily: bcr protein
C:Keywords: ATP; molecular chaperone

Query Match 11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 7.1e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 HLKQEI 16
|||
DB 23 HGKVEI 28

RESULT 37
B54127
dolichyl-diphosphooligosaccharide-protein glycotransferase (EC 2.4.1.119) 65k chain I - c
N:Alternate names: oligosaccharyltransferase
C:Species: Gallus gallus (chicken)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: B54127
R:Kumar, V.; Heinemann, F.S.; Ozols, J.
J. Biol. Chem. 269, 13451-13457, 1994
A:Title: Purification and characterization of avian oligosaccharyltransferase. Complete
A:Reference number: A54127; MUID:94230453; PMID:8175777
A:Accession: B54127
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-28 <KUM>
A:Cross-references: UNIPROT:P80896; UNIPARC:UPI0000130EC4
C:Superfamily: Caenorhabditis elegans hypothetical protein T22D1.4
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WK 8
||
DB 22 WK 23

RESULT 38
T06340
ribosomal protein S16 - soybean chloroplast (fragment)
C:Species: chloroplast Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06340
R:Nielsen, N.C.
submitted to the EMBL Data Library, May 1995
A:Reference number: Z15613
A:Accession: T06340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-28 <NIE>
A:Cross-references: UNIPROT:Q32307; UNIPARC:UPI000008B5A1; EMBL:U26948; NID:g984307; PIDN:
A:Experimental source: cultivar Resnik; leaf
C:Genetics:
A:Gene: rps16
A:Genome: chloroplast
C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match 11.7%; Score 16; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KW 7
||
DB 22 KW 23

RESULT 39
S66436
allophycocyanin alpha-B chain - Anabaena sp. (strain PCC 7120) (fragment)
C:Species: Anabaena sp.
A:Variety: PCC 7120
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66436
R:Ducret, A.; Sidler, W.; Wehrli, E.; Frank, G.; Zuber, H.
Eur. J. Biochem. 236, 1010-1024, 1996

```

Query Match      10.9%; Score 15; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 9.1e+04;
Matches 1; Conservative . 2; Mismatches 0; Indels 0; Gaps 0;

Qy      6 KWK 8
        :|:
Db      23 RWR 25

RESULT 42

```

QY 1 KIPALKWKN 9
 || : || :
 Db 4 KIPLVKKS 12

RESULT 45

PC2239
 heat shock protein, high-molecular-mass 105B - mouse (fragments)
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 17-Mar-1999
 C:Accession: PC2239
 R:Hatayama, T.; Yasuda, K.; Nishiyama, E.
 Biochem. Biophys. Res. Commun. 204, 357-365, 1994
 A:Title: Characterization of high-molecular-mass heat shock proteins and 42oC-specific h
 A:Reference number: PC2238; MUID:95032120; PMID:7945382
 A:Accession: PC2239
 A:Molecule type: protein
 A:Residues: 1-28 <HAT>
 A:Cross-references: UNIPARC:UPI000017C679
 C:Keywords: heat shock; stress-induced protein

Query Match 10.9%; Score 15; DB 2; Length 28;
 Best Local Similarity 40.0%; Pred. NO. 9.1e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 16 IAALE 20
 :|||
 Db 4 VSAIE 8

Search completed: November 21, 2005, 21:47:33
 Job time : 24.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 21:26:34 ; Search time 142 Seconds
(without alignments)
139.118 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIRALKWNAHLKQETAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1678

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	22.6	28	Q4SXA6_TETNG	Q4SXA6 tetraodon n
2	30	21.9	28	Q9IN95_9HIV1	Q9in95 human immun
3	29	21.2	28	Q4XP22_PLACH	Q4xpp2 plasmodium
4	29	21.2	28	Q4TT22_9SPHN	Q4tt22 erythroblast
5	28	20.4	28	Q4RCL2_TETNG	Q4rcl2 tetraodon n
6	27	19.7	28	Q4YD65_PLABE	Q4yd65 plasmodium
7	27	19.7	28	Q4TIF5_TETNG	Q4tif5 tetraodon n
8	26	19.0	28	Q8ZYV3_PVRAB	Q8zyv3 pyrobaculum
9	26	19.0	28	Q7GHK5_AEDAL	Q7ghk5 ades albop
10	26	19.0	28	Q4Z2J3_PLABE	Q4z2j3 plasmodium
11	26	19.0	28	Q6AGW8_LEIXX	Q6agw8 leifsonia x
12	25	18.2	28	Q9TWV5_PERAM	Q9twv5 periplaneta
13	25	18.2	28	Q4X6M9_PLACH	Q4x6m9 plasmodium
14	25	18.2	28	Q4XC08_PLACH	Q4xc08 plasmodium
15	24	17.5	28	Q6U7R1_CRYNV	Q6u7r1 cryptococcus
16	24	17.5	28	Q00440_GLOLA	Q00440 glomerella
17	24	17.5	28	Q2TW22_PARLI	Q2tw22 paracentrot
18	24	17.5	28	Q99LW3_MOUSE	Q99lw3 mus musculu
19	24	17.5	28	Q4LT3N5_TETNG	Q4lt3n5 tetraodon n
20	23	16.8	28	Q53TM9_HUMAN	Q53tm9 homo sapien
21	23	16.8	28	Q4XCS0_PLACH	Q4xcso plasmodium
22	23	16.8	28	Q4YAC7_PLABE	Q4yac7 plasmodium
23	23	16.8	28	Q94IS1_PINRA	Q94is1 pinus radia
24	23	16.8	28	Q4NC96_9WICC	Q4nc96 arthrobaete
25	23	16.8	28	Q8X415_ECO57	Q8x415 escherichia
26	23	16.8	28	Q91VP0_MOUSE	Q91vp0 mus musculu
27	22	16.1	28	Q7S105_NEUCR	Q7s105 neurospora
28	22	16.1	28	P87021_MAGGR	P87021 magnaportha
29	22	16.1	28	Q4Y377_PLACH	Q4y377 plasmodium
30	22	16.1	28	Q4YE24_PLABE	Q4yez4 plasmodium
31	22	16.1	28	Q4YQ52_PLABE	Q4yq52 plasmodium

32 22 16.1 28 2 Q4Z0C3_PLABE
33 22 16.1 28 2 Q62731_CANFA
34 22 16.1 28 2 Q9GMF5_PAPHA
35 22 16.1 28 2 Q9GMF6_MACMU
36 22 16.1 28 2 Q9XGE6_VICFA
37 22 16.1 28 2 Q50102_MYCLE
38 22 16.1 28 2 Q93JY6_MYCTF
39 22 16.1 28 2 Q724A1_LIISM
40 22 16.1 28 2 Q4RFB7_TETNG
41 22 16.1 28 2 Q4SVA3_TETNG
42 21.5 15.7 28 2 Q5F210_MOUSE
43 21 15.3 28 1 GRP_ALLEMI
44 21 15.3 28 2 Q5AW44_EMENT
45 21 15.3 28 2 Q9TWX0_MANSE

Q4Z0C3 plasmodium
Q62731 canis famil
Q9GMF5 papio hanad
Q9GMF6 macaca mula
Q9XGE6 vicia faba
Q50102 mycobacteri
Q93JY6 mycobacteri
Q724A1 listeria mo
Q4RFB7 tetraodon n
Q4SVA3 tetraodon n
Q5F210 mus musculu
P87021 alligator m
Q5AW44 aspergillus
Q9TWX0 manduca sex

ALIGNMENTS

RESULT 1
Q4SXA6_TETNG
ID Q4SXA6_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4SXA6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAP12653, whole genome shotgun sequence.
DE (Fragment).

OS ORFNames=GSTENG00011027001;
GN Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Creaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McGowan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RG Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAB01012653; CAP94726.1; -; Genomic_DNA.
DR NON TER 28 28
SQ SEQUENCE 28 AA; 3511 MW; 48861A48ADBFB624 CRC64;

Query Match 22.6%; Score 31; DB 2; Length 28;
Best Local Similarity 55.6%; Pred. No. 8.4e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIRALKWKN 9
Db 6 QURLLLWKN 14

RESULT 2

QY 5 LKWNAHLKQE 15
.:|.:|:

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RP NUCLEOTIDE SEQUENCE
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01018625; CAG13871.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 28 AA; 3067 MW; 5BEFD973E2BD15CF CRC64;

Query Match 20.4%; Score 28; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQEI 17
Db 9 RWGTCHPKPELS 20

RESULT 6
Q4YD65_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YD65;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB406027.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RA transcriptomic, and proteomic analyses.";
RL Science 307:82-86 (2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAR1006329; CAI04054.1; -; Genomic_DNA.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3374 MW; 3778B93D36F8559C CRC64;

Query Match 19.7%; Score 27; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 WKNAHL 12
Db 12 WENLHI 17

RESULT 7
Q4TIF5_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4TIF5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF2190, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00038313001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

```

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OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; CAAE01002190; CAF87327.1; -; Genomic_DNA.
DR NON TER 28
FT NON TER 28
SQ SEQUENCE 28 AA; 3040 MW; 776D95631570A999 CRC64;

Query Match 19.7%; Score 27; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.8e+04;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 10 AHLKQETIALEQEI 24
Db 11 AEVRKLALELELS 25

RESULT 8
Q8ZY3_PYRAE PRELIMINARY; PRT; 28 AA.
AC Q8ZY3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE0551.
GN OrderedLocustNames=PAE0551;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
DR EMBL; AE009773; AAL62858.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3001 MW; 869F81422C93A14D CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 29.4%; Pred. No. 3.7e+04;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 10 AHLKQETIALEQEI 26
Db 4 AEIKASVAELKAVGSL 20

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RESULT 9
Q7GHK5 AEDAL
ID Q7GHK5 AEDAL PRELIMINARY; PRT; 28 AA.
AC Q7GHK5
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Aedes albopictus (Forest day mosquito).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Culicinae; Culicini; Aedes; Stegomyia.
OX NCBI_TaxID=7160;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84307776; PubMed=6477610;
RA Heuchlen C.C., Dublin D.T.;
RL "A cluster of four transfer RNA genes in mosquito mitochondrial DNA.";
RL Biochem. Int. 8:385-391(1984).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 3 family.
DR ENBL; M27317; AAA65504.2; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR InterPro; IPR000440; Oxidored_q4.
DR Pfam; PF00507; Oxidored_q4; 1.
DR Hypothetical protein; Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
KW NON TER
FT NON TER
SQ SEQUENCE 28 AA; 3340 MW; BAFCF50953E376FF CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 3.7e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ALKWN 9
Db 23 ALEWNN 28

RESULT 10
Q42ZJ3 PLABE
ID Q42ZJ3 PLABE PRELIMINARY; PRT; 28 AA.
AC Q42ZJ3
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB102380.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CRAI01000932; CAH95494.1; -; Genomic_DNA.
DR EMBL; CRAI01000932; CAH95494.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 28 AA; 3512 MW; 8CD8C5CFE90006F6 CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 41.7%; Pred. No. 3.7e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 ALKWNHLKOE 15
Db 8 ALNYNEARLKDD 19

RESULT 11
Q6AGW8 LEIXX
ID Q6AGW8 LEIXX PRELIMINARY; PRT; 28 AA.
AC Q6AGW8;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LXX03670;
OS Leifsonia xyl (subsp. xyl).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
xyl subsp. xyl.";
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT88377.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3119 MW; 79BD5C47B0248C77 CRC64;

Query Match 19.0%; Score 26; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 3.7e+04;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 WKNHLKOEIAL 19
Db 13 YKIIHKNALAF 25

RESULT 12
Q9TWV5 PERAM
ID Q9TWV5 PERAM PRELIMINARY; PRT; 28 AA.
AC Q9TWV5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 10 kDa LEG regeneration protein (Fragment).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Blattinae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93075619; PubMed=1445782;
RA Nomura A., Kawasaki K., Kubo T., Natori S.;
RT "Purification and localization of p10, a novel protein that increases
in nymphal regenerating legs of Periplaneta americana (American
cockroach).";

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RL Int. J. Dev. Biol. 36:391-398(1992).
DR HSP; Q9NG96; INSV.
DR InterPro; IPR005055; A10_OS-D.
DR Pfam; PF03392; OS-D; 1.
SQ SEQUENCE 28 AA; 3367 MW; B0BEF9AD586758B7 CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 5e+04;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 6 KWKNAHLKQRIIA 18
Db 7 KYDNIKKEILAS 19

RESULT 13
Q4X6M9_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4X6M9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC405735.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01009461; CAH87447.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3469 MW; C55F38F38D3D91D5 CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 5e+04;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQBI 16
Db 5 KRKYKKKLYKWDI 20

RESULT 14
Q4XCC8_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4XCC8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC403471.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

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RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01007638; CAH85444.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3294 MW; 80691A982EC6A73B CRC64;

Query Match 18.2%; Score 25; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 5e+04;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQ 14
Db 11 KIKNLNTSCAHTKK 24

RESULT 15
Q6U7R1_CRYNV PRELIMINARY; PRT; 48 AA.
AC Q6U7R1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE C-24 sterol reductase (Fragment).
GN Name=ERG4;
OS Cryptococcus neoformans var. grubii H99.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
CX NCBI_TaxID=235443;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99;
RA Stuart L.T., Allen A., Dietrich F.S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY376721; AAQ88132.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR001171; ERG4_ERG24.
DR Pfam; PF01222; ERG4_ERG24; 1.
FT NON TER 1
SQ SEQUENCE 28 AA; 3430 MW; E645861ED8FF19DC CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.7e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RALKWK 8
Db 17 KVKWK 22

RESULT 16
Q00440_GLOLA PRELIMINARY; PRT; 48 AA.
ID Q00440_GLOLA PRELIMINARY;
AC Q00440;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAS protein (Fragment).
GN Name=Cirasi;
OS Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
OS lagenarium).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
CX NCBI_TaxID=5462;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC TISSUE=Mycelium;
RA Lee C.-W., Kim J.-S., Jung B.-K., Park S.-H.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U33745; AAA74985.1; -; Genomic_DNA.
DR HSSP: P01112; 1PLK.
DR GO: GO:000525; F:GTP binding; IEA.
DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR Pfam; PF00071; Ras; 1.
KW GTP-binding; Nucleotide-binding.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3189 MW; 77197F0558CAAADC CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 6.7e+04;
Matches 5; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 9 NAHLKQEIQAALQEIQAAL 27
   ::: ||| :||| :|
Db 1 DSYRKQ--CVIDEVALLD 17

RESULT 17
Q9TWE2_PARLI PRELIMINARY; PRT; 28 AA.
AC Q9TWE2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE AXONEMAL alpha-tubulin isoform (fragment).
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7656;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=96215272; PubMed=8626623; DOI=10.1074/jbc.271.17.9928;
RA Mary J., Redeker V., Le Caer J.P., Rossier J., Schmitter J.M.;
RT "Posttranslational modifications in the C-terminal tail of axonemal
RT tubulin from sea urchin sperm".
RL J. Biol. Chem. 271:9928-9933(1996).
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alpha tubulin.
DR PANTHER; PTHR11588:SF1; Alpha tubulin; 1.
SQ SEQUENCE 28 AA; 3104 MW; 9C50E220D1AFD7C1 CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 6.7e+04;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 EIAALQEQE 22
   :|||::|
Db 1 DLAALEKD 8

RESULT 18
Q99LW3_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q99LW3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypochemical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002195; AAH02195.1; -; mRNA.
KW Ensembl; ENSMUSG0000057032; Mus musculus.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 3503 MW; 737D5EC9A6E6CFD9B CRC64;

Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 23.1%; Pred. No. 6.7e+04;
Matches 3; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRALKWKNAHLKQ 14
   :|||:
Db 12 VTTLWRAGNYEQ 24

RESULT 19
Q4T3N5_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4T3N5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF978, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00007715001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fieher S., Lutfalla G., Dossat C., Segrens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blement C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigou R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudat V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

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RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype."; Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01009978; CAP92497.1; -; Genomic_DNA.
FT NON_TER 1 28
FT NON_TER 28
SQ SEQUENCE 28 AA; 3037 MW; 996533BD98146314 CRC64;
Query Match 17.5%; Score 24; DB 2; Length 28;
Best Local Similarity 31.2%; Pred. No. 6.7e+04;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 12 LKQEIATLEQEIATLE 27
Db 3 LREAVALLTAQQTSL 18
RESULT 20
Q53TM9 HUMAN PRELIMINARY; PRT; 28 AA.
AC Q53TM9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein FLJ13984 (fragment).
GN Name=FLJ13984;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Walker C., Drone K., Page K.;
RA "The sequence of Homo sapiens BAC clone RP11-284E18.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008065; AAX93077.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 28
SQ SEQUENCE 28 AA; 3288 MW; BDBE4ACFFC20A84D CRC64;
Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 8.9e+04;
Matches 5; Conservative 6; Mismatches 4; Indels 4; Gaps 1;
Qy 5 LKWKNAHLKQEIATLEQEI 23
Db 1 MOWS-----KEEAAARKKV 15
RESULT 21
Q4XCS0 PLACH PRELIMINARY; PRT; 28 AA.
ID Q4XCS0 PLACH

AC Q4XCS0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC403293.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemodsporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAJ01007505; CAH85302.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 28 AA; 2982 MW; 1ED93C8890D0D509 CRC64;
Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 41.2%; Pred. No. 8.9e+04;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
Qy 11 HLKQEIATLEQEIATLE 27
Db 9 NLVEESLALLKEIYLCE 25
RESULT 22
Q4YAC7 PLABE PRELIMINARY; PRT; 28 AA.
ID Q4YAC7 PLABE
AC Q4YAC7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB401815.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemodsporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RL transcriptomic, and proteomic analyses."; Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAT01007122; CAI05297.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 28 AA; 3288 MW; 52CB801BB1CD1F21 CRC64;
Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 41.7%; Pred. No. 8.9e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KIRALKWKNAHL 12

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Db          || : || | :
13 KITLIKHGARI 24

RESULT 23
Q941S1_PINRA
ID Q941S1_PINRA PRELIMINARY; PRT; 28 AA.
AC Q941S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nonspecific lipid transfer protein (Fragment).
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jones D.F.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029020; AAK40292.1; -; Genomic_DNA.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2989 MW; 89853214D0F658B6 CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 WRNVAHL 12
DB 3 WKAANL 8

RESULT 24
Q4NC96_9MICC
ID Q4NC96_9MICC PRELIMINARY; PRT; 28 AA.
AC Q4NC96;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ArthDRAFT_0836;
OS Arthrobaacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococccaceae; Arthrobaacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA US DOE Joint Genome Institute (PGF-ORNL);
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pfluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobaacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA US DOE Joint Genome Institute (PGF-ORNL);
RC STRAIN=FB24;
RG Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Arthrobaacter sp. FB24."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHQ01000016; EAL95000.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 2977 MW; 89C905D398BE0BA4 CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 18 ALEQETIAALE 27
DB 18 ATEETSLLUE 27

RESULT 26
Q91VP0_MOUSE
ID Q91VP0_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q91VP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=Mobk1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 17 AALEQETIAAL 26
DB 13 AATEAKIRAL 22

RESULT 25
Q8X415_ECO57
ID Q8X415_ECO57 PRELIMINARY; PRT; 28 AA.
AC Q8X415;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=z3917;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Ferris N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
DR EMBL; AE005174; AAG57732.1; -; Genomic_DNA.
DR PIR; H85908; H85908.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 28 AA; 3099 MW; DAFD94CC752FF0B0 CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 18 ALEQETIAALE 27
DB 18 ATEETSLLUE 27

RESULT 26
Q91VP0_MOUSE
ID Q91VP0_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q91VP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=Mobk1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
RA Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011285; AAH11285.1; -; mRNA.
DR MGI; MGI:2442631; Mobk1b.
KW Hypothetical protein.
SQ SEQUENCE 28 AA; 2809 MW; 97A97BBE33A3F19F CRC64;

Query Match 16.8%; Score 23; DB 2; Length 28;
Best Local Similarity 33.3%; Pred. No. 8.9e+04;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 16 IAALQEIAALE 27
DB :||: :||:
9 LAAPRQYGALD 20

RESULT 27
Q7S105_NEUCR
ID Q7S105_NEUCR PRELIMINARY; PRT; 28 AA.
AC Q7S105;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU00647.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M., Schulte U.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeiter A., Greenberg D.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyskellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannheimaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC CC
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABX0100001; EAA36551.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3235 MW; C3CD3869AFC94760 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 HLKQEI1A 18

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Db 5 HLKHAVRA 12
||| :|
P87021_MAGGR PRELIMINARY; PRT; 28 AA.
ID P87021;
AC P87021;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RAS protein (Fragment).
GN Name=MGRAS1;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-6; TISSUE=Mycelium;
RX MEDLINE=97306448; PubMed=9163749;
RA Park S.Y., Lee E.J., Lee C.W.;
RT "Molecular cloning and sequence analysis of a putative ras gene of the
RT phytopathogenic fungus Botryotinia fuckeliana.";
RL Mol. Cells 7:300-304(1997).
DR EMBL; U79559; AAB51237.1; -; Genomic_DNA.
DR HSSP; P01112; 1PLK.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras_trnsfrmg.
DR Pfam; PF00071; Ras; 1.
DR GTP-binding; Nucleotide-binding.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3175 MW; 7718A47586CAADC CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 26.3%; Pred. No. 1.2e+05;
Matches 5; Conservative 7; Mismatches 5; Indels 2; Gaps 1;

QY 9 NAHLKQEI1AALQEI1AAL 27
DB :||: :||:
1 DSYRKQ-CVIDDEVALLD 17

RESULT 29
Q4Y377_PLACH
ID Q4Y377_PLACH PRELIMINARY; PRT; 28 AA.
AC Q4Y377;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PCI02434.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC CC
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAJ01001405; CAH76383.1; -; Genomic_DNA.
KW Hypothetical protein.

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FT NON TER 1
SQ SEQUENCE 28 AA; 3439 MW; 8F5EBB75272F8B4C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 KNAHL 12
DB 9 RNAHI 13

RESULT 30
Q4YE24_PLABE
ID Q4YE24_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YE24;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB404883.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3491 MW; A2D2C1861CEDF94C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WKNAH 11
DB 15 WKSAN 19

RESULT 31
Q4YQS2_PLABE
ID Q4YQS2_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4YQS2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB107544.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";

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RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAI01002911; CAH99635.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 28
SQ SEQUENCE 28 AA; 3252 MW; 40E0D8480B5DFA21 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 WKNAH 11
DB 17 YKNSH 21

RESULT 32
Q4Z0C3_PLABE
ID Q4Z0C3_PLABE PRELIMINARY; PRT; 28 AA.
AC Q4Z0C3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB103349.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 28 AA; 3430 MW; 2C2E6C5C95CCB88E CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 57.1%; Pred. No. 1.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 KWKNAHL 12
DB 12 KKNHI 18

RESULT 33
O62731_CANFA
ID O62731_CANFA PRELIMINARY; PRT; 28 AA.
AC O62731;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Tropomyosin (fragment).
GN Name=TPM1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;

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RN NUCLEOTIDE SEQUENCE.
RP Liu P.-C., Chen Y.-W., Grob S.E., Katz M.L., Johnson G.S.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049587; AAC05499.1; -; Genomic DNA.
DR Ensembl; ENSCAPG0000016966; Canis familiaris.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin, 1.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3251 MW; 5694A77F1CA73D30 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 36.4%; Pred. No. 1.2e+05;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 13 LKQETAALEQEI 23
Db 12 ESKCAELEEL 22

RESULT 34
Q9GMF5 PAPHA PRELIMINARY; PRT; 28 AA.
AC Q9GMF5
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Rh50 glycoprotein (Fragment).
GN Name=RHAG;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Papio.
OX NCBI_TaxID=95557;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363873; PubMed=10903374;
RA Huang C.H., Liu Z., Apoll P.A., Blancher A.;
RT "Sequence, organization, and evolution of Rh50 glycoprotein genes in
nonhuman primates.";
RL J. Mol. Evol. 51:76-87(2000).
DR EMBL; AF177632; AAG00314.1; -; Genomic DNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 3332 MW; EB74D4E45F83A90C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQETAALEQEI 26
Db 3 LKFLPMAIVLEIAMI 17

RESULT 35
Q9GMF6 MACMU PRELIMINARY; PRT; 28 AA.
AC Q9GMF6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Rh50 glycoprotein (Fragment).
GN Name=RHAG;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20363873; PubMed=10903374;
RA Huang C.H., Liu Z., Apoll P.A., Blancher A.;
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RT "Sequence, organization, and evolution of Rh50 glycoprotein genes in
nonhuman primates.";
RL J. Mol. Evol. 51:76-87(2000).
DR EMBL; AF177631; AAG00313.1; -; Genomic DNA.
FT NON_TER 28
SQ SEQUENCE 28 AA; 3332 MW; EB74D4E45F83A90C CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LKQETAALEQEI 26
Db 3 LKFLPMAIVLEIAMI 17

RESULT 36
Q9XGE6 VICFA PRELIMINARY; PRT; 28 AA.
AC Q9XGE6
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Ribonuclease H (fragment).
GN Name=RNase H;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Pearce S.R., Stuart-Rogers C., Knox M., Kumar A., Ellis T.H.,
RA Flavell A.J.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243100; CAB45144.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 28 AA; 3265 MW; AA26A6A8F2F280D6 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.2e+05;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 12 LKQETAALEQEI 23
Db 16 IRRELGLDNKI 27

RESULT 37
Q50102 MYCLE PRELIMINARY; PRT; 48 AA.
AC Q50102
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE U650k.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15184; AAA63067.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3515 MW; F732EAA1A754562 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 21.4%; Pred. No. 1.2e+05;
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Matches 3; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 2 IRALKWNAHLKOE 15
Db 12 LRHLRQHRRHVRD 25

RESULT 38
Q93JY6 MYCTU
ID Q93JY6_MYCTU PRELIMINARY; PRT; 28 AA.
AC Q93JY6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DNA-directed RNA polymerase (Fragment).
GN Names=rpob;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21367865; PubMed=11474030;
RX DOI=10.1128/JCM.39.8.2987-2990.2001;
RA Mani C., Selvakumar N., Narayanan S., Narayanan P.R.;
RT "Mutations in the rpoB gene of multidrug-resistant Mycobacterium
tuberculosis clinical isolates from India.";
RL J. Clin. Microbiol. 39:2987-2990(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Chervu M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ297928; CAC50349.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006350; F:transcription; IEA.
DR InterPro; IPR007645; RNA_pol_Rpb2_3.
DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
KW DNA-directed RNA polymerase.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3129 MW; 64E6333409DFD446 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 13 KQBIAALE 20
Db 21 KRLSLALE 28

RESULT 39
Q724A1 LISMF
ID Q724A1_LISMF PRELIMINARY; PRT; 28 AA.
AC Q724A1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=LMOF2365_0323;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
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RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Iran B., Kathariou S., Wonderling L.D., Unlich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AB017323; AAT03110.1; -; Genomic_DNA.
DR TIGR; LMOF2365_0323; -.
KW Complete proteome.
SQ SEQUENCE 28 AA; 3243 MW; E699E78C805C13B9 CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 50.0%; Pred. No. 1.2e+05;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 12 LKQETAAALQEI 23
Db 1 MKLLFATLVEI 12

RESULT 40
Q4RFB7 TETNG
ID Q4RFB7_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4RFB7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 8 SCAP15119, whole genome shotgun sequence.
GN ORFNames=GSTENG00035394001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chaplie C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE0105119; CAG12915.1; -; Genomic_DNA.
SQ SEQUENCE 28 AA; 2884 MW; 3755B80F01ADC3D3D CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 66.7%; Pred. No. 1.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 IRALKW 7
Db 10 ITALSW 15

RESULT 41
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Q4SVA3_TETNG
ID Q4SVA3_TETNG PRELIMINARY; PRT; 28 AA.
AC Q4SVA3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF13770, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG00012080001;
GN Tetraodon nigroviridis (Green puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA David C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01013770; CAF95429.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3250 MW; C50C59229401CF6D CRC64;

Query Match 16.1%; Score 22; DB 2; Length 28;
Best Local Similarity 37.5%; Pred. No. 1.2e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 ALKWKNAH 11
| : |
| : |
Db 4 AKWESEPH 11

RESULT 42
Q5F210_MOUSE
ID Q5F210_MOUSE PRELIMINARY; PRT; 28 AA.
AC Q5F210;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Oxytocin binding protein 2 (Fragment).
GN Name=Osbp2; ORFNames=RP23-309E11.7-004;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Dunn M.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731853; CAI51856.1; -; Genomic_DNA.
FT NON_TER 28 28

SQ SEQUENCE 28 AA; 3453 MW; 2BF5DACD2D68FCFC CRC64;

Query Match 15.7%; Score 21.5; DB 2; Length 28;
Best Local Similarity 45.5%; Pred. No. 1.4e+05;
Matches 5; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 6 KWKNA-HLKQE 15
| : |
| : |
Db 18 KWQRALNYEQE 28

RESULT 43
GRP_ALIMI
ID GRP_ALIMI STANDARD; PRT; 28 AA.
AC P3186;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gastrin-releasing peptide (GRP) [Contains: Neuromedin C (GRP-10)].
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369; DOI=10.1016/0196-9781(93)90147-9;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RL and stomach of the alligator.";
RL Peptides 14:573-579(1993).
CC -! FUNCTION: GRP stimulates gastrin release as well as other
CC gastrointestinal hormones.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC InterPro: IPR000874; Bombesin.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amidation; Bombesin family; Direct protein sequencing.
FT PEPTIDE 19 28 Neuromedin C.
FT MOD_RES 28 28 Methionine amide.
SQ SEQUENCE 28 AA; 2786 MW; A74DB0487D844963 CRC64;

Query Match 15.3%; Score 21; DB 1; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 RALKWKNAHL 12
| : |
| : |
Db 18 RGSWAVGHL 27

RESULT 44
Q5AW44_EMENI
ID Q5AW44_EMENI PRELIMINARY; PRT; 28 AA.
AC Q5AW44;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Predicted protein.
GN ORFNames=AN7486.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eutiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearrellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACD01000129; EAA62066.1; -; Genomic DNA.
SQ SEQUENCE 28 AA; 3333 MW; 47DC557430549950 CRC64;

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 25.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 8 KNAHLKQE 15
Db 16 RDGHIRQ 23

RESULT 45
Q9TWX0 MANSE
ID Q9TWX0 MANSE PRELIMINARY; PRT; 28 AA.
AC Q9TWX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cell surface protein 2F5 91 kDa component (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92331807; PubMed=1628754;
RA Nardi J.B.;
RT "Dynamic expression of a cell surface protein during rearrangement of
RT epithelial cells in the Manduca wing monolayer.";
RL Dev. Biol. 152:161-171(1992).
DR PIR; A44877; A44877. 1
FT NON_TER 1
FT TER 28 28
SQ SEQUENCE 28 AA; 3271 MW; 28D250E730959651 CRC64;

Query Match 15.3%; Score 21; DB 2; Length 28;
Best Local Similarity 27.8%; Pred. No. 1.6e+05;
Matches 5; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 7 WKNA---HLKQRIAALE 20
Db 5 WRVADESLEVEKQIESFE 22

Search completed: November 21, 2005, 21:46:24
Job time : 144 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 21:25:48 ; Search time 31.5 Seconds
(without alignments)
73.489 Million cell updates/sec

Title: US-10-088-417A-4
Perfect score: 137
Sequence: 1 KIPALKWNAHLKQETALRQETAALEQ 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 4644

Minimum DB seq length: 28
Maximum DB seq length: 28

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	32.8	28	2	US-08-486-099-84
2	45	32.8	28	2	US-08-360-107A-94
3	45	32.8	28	2	US-08-484-223B-84
4	45	32.8	28	2	US-08-919-597-84
5	45	32.8	28	2	US-08-475-668A-84
6	45	32.8	28	2	US-08-485-551A-84
7	45	32.8	28	2	US-08-471-913A-84
8	45	32.8	28	2	US-08-485-264A-84
9	45	32.8	28	2	US-08-474-349A-84
10	45	32.8	28	2	US-08-255-208A-20
11	45	32.8	28	2	US-08-470-896-84
12	45	32.8	28	2	US-09-914-259-1
13	45	32.8	28	2	US-08-485-546A-84
14	45	32.8	28	2	US-09-350-841A-1549
15	45	32.8	28	2	US-09-350-841A-1566
16	45	32.8	28	2	US-09-350-841A-1573
17	45	32.8	28	2	US-08-487-266A-84
18	45	32.8	28	2	US-08-484-741-84
19	44	32.1	28	1	US-08-182-175A-1
20	44	32.1	28	1	US-08-182-175A-3
21	38	27.7	28	1	US-08-474-633A-70
22	38	27.7	28	1	US-08-823-771-70
23	38	27.7	28	4	PCT-US92-06412-3
24	38	27.7	28	4	PCT-US92-06412-3
25	37	27.0	28	1	US-07-977-630-53
26	36	26.3	28	1	US-08-182-175A-2
27	36	26.3	28	1	US-08-182-175A-39

28	28	26.3	28	1	US-08-182-175A-43	Sequence 43, Appl
29	36	26.3	28	1	US-08-182-175A-47	Sequence 47, Appl
30	36	26.3	28	1	US-08-474-633A-36	Sequence 36, Appl
31	36	26.3	28	1	US-08-474-633A-40	Sequence 40, Appl
32	36	26.3	28	1	US-08-474-633A-56	Sequence 56, Appl
33	36	26.3	28	1	US-08-474-633A-67	Sequence 67, Appl
34	36	26.3	28	1	US-08-944-133-18	Sequence 18, Appl
35	36	26.3	28	2	US-08-823-771-36	Sequence 36, Appl
36	36	26.3	28	2	US-08-823-771-40	Sequence 40, Appl
37	36	26.3	28	2	US-08-823-771-56	Sequence 56, Appl
38	36	26.3	28	2	US-08-823-771-67	Sequence 67, Appl
39	36	26.3	28	4	PCT-US92-06412-2	Sequence 2, Appl
40	36	26.3	28	4	PCT-US92-06412-39	Sequence 39, Appl
41	36	26.3	28	4	PCT-US92-06412-43	Sequence 43, Appl
42	36	26.3	28	4	PCT-US92-06412-47	Sequence 47, Appl
43	35	25.5	28	1	US-08-944-133-31	Sequence 31, Appl
44	35	25.5	28	1	US-08-944-133-35	Sequence 35, Appl
45	35	25.5	28	2	US-09-082-279B-377	Sequence 377, App

ALIGNMENTS

RESULT 1
US-08-486-099-84
; Sequence 84, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-486-099-84

Query Match 32.8%; Score 45; DB 2; Length 28;

Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 2

US-08-360-107A-94
; Sequence 94, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-360-107A-94

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 3

US-08-484-223B-84
; Sequence 84, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 4

US-08-919-597-84
; Sequence 84, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

QY 1 KIRALKWKNHLEKQIAALEQ 21
|:| ||| |:| |:| |:| |:|
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 7

US-08-471-913A-84
; Sequence 84, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 84:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-913A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLEKQIAALEQ 21
|:| ||| |:| |:| |:| |:|
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 8

US-08-485-264A-84
; Sequence 84, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-485-264A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLEKQIAALEQ 21
|:| ||| |:| |:| |:| |:|
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 9

US-08-474-349A-84
; Sequence 84, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-474-349A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 11
US-08-470-896-84
; Sequence 84, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-470-896-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-474-349A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKOEIAALEQ 21
Db 7 KVEELLSKNYHLENEVARLKK 27

RESULT 10
US-08-255-208A-20
; Sequence 20, Application US/08255208A
; Patent No. 6440856
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
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RESULT 12
US-09-914-259-1
; Sequence 1, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-914-259-1

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 7; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 13
US-08-485-546A-84
; Sequence 84, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING BPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 7; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 14
US-09-350-841A-1549
; Sequence 1549, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1549
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1549

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 7; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 15
US-09-350-841A-1566
; Sequence 1566, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1566
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1566

Query Match      32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 7; Gaps 0;

QY      1 KIRALKWKNAHLKQETAALEQ 21
       |:| ||| |:| |:| |:|
Db      7 KVEELLSKNYHLENEVARLKK 27

RESULT 16
US-09-350-841A-1573
; Sequence 1573, Application US/09350841A
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; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1573
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1573

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKOEIAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 17
US-08-487-266A-84
; Sequence 84, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-266A-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKOEIAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 18

US-08-484-741-84
; Sequence 84, Application US/08484741
; Patent No. 6951717
; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION

; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,741
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-08-484-741-84

Query Match 32.8%; Score 45; DB 2; Length 28;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKOEIAALEQ 21
|:| |||:|:|:
Db 7 KVEELLSKNVHLENEVARLKK 27

RESULT 19

US-08-182-175A-1
; Sequence 1, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:

```
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION/DOCKET NUMBER: BB-1031
; REFERENCE/DOCKET NUMBER: 33,692
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4)4"
; PCT-US92-06412-1
;
; Query Match 32.1%; Score 44; DB 1; Length 28;
; Best Local Similarity 36.0%; Pred. No. 22;
; Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
;
QY 1 KIRALKWNAHLKQETAALEQETAA 25
   |::||:| |::||:| |::||:|
Db 4 KLKALEEKLKALEEKLKALEEKLKA 28

RESULT 20
PCT-US92-06412-1
; Sequence 1, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
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; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION/DOCKET NUMBER: BB-1031
; REFERENCE/DOCKET NUMBER: 33,692
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 4)4"
; PCT-US92-06412-1
;
; Query Match 32.1%; Score 44; DB 4; Length 28;
; Best Local Similarity 36.0%; Pred. No. 22;
; Matches 9; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
;
QY 1 KIRALKWNAHLKQETAALEQETAA 25
   |::||:| |::||:| |::||:|
Db 4 KLKALEEKLKALEEKLKALEEKLKA 28

RESULT 21
US-08-182-175A-3
; Sequence 3, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
```

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; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7)4"
US-08-182-175A-3

Query Match      27.7%; Score 38; DB 1; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQBIALEQEIAA 25
        |::|::| :|::| :|::| :|::|
DB      4 KLKAMEEKLKAMEEKLKAMEEKLA 28

RESULT 22
US-08-474-633A-70
; Sequence 70, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7)4"
US-08-823-771-70

Query Match      27.7%; Score 38; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQBIALEQEIAA 25
        |::|::| :|::| :|::| :|::|
DB      4 KLKAMEEKLKAMEEKLKAMEEKLA 28

RESULT 23
US-08-823-771-70
; Sequence 70, Application US/08823771
; Patent No. 6459019
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,771
; FILING DATE: 24-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/474,633
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7)4"
US-08-823-771-70

Query Match      27.7%; Score 38; DB 2; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKWNAHLKQBIALEQEIAA 25
        |::|::| :|::| :|::| :|::|
DB      4 KLKAMEEKLKAMEEKLKAMEEKLA 28

RESULT 24
US-08-474-633A-70
; Sequence 70, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,633A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

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Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETIALEQETAA 25
|::||:| ::::|::||:|
Db 4 KLKAMEBKLKAMEBKLKAMEBKLKA 28

RESULT 24

PCT-US92-06412-3
; Sequence 3, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 7)4"
PCT-US92-06412-3

Query Match 27.7%; Score 38; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQETIALEQETAA 25
|::||:| ::::|::||:|
Db 4 KLKAMEBKLKAMEBKLKAMEBKLKA 28

RESULT 25

US-07-977-630-53
; Sequence 53, Application US/07977630
; Patent No. 5583038
; GENERAL INFORMATION:
; APPLICANT: Stover, Charles K.
; TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING

; TITLE OF INVENTION: DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,630
; FILING DATE: No. 5583038ember 17, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 469201-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-977-630-53
Query Match 27.0%; Score 37; DB 1; Length 28;
Best Local Similarity 56.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 11 HLKQETIALEQETIAAL 26
||| :|||
Db 5 HLALETAMRQETIAL 20

RESULT 26

US-08-182-175A-2
; Sequence 2, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:

US-08-182-175A-47
; Sequence 47, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice

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	US-08-944-133-18	Query Match Best Local Similarity 26.3%; Score 36; DB 1; Length 28; Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY	2 IRALKKNAHLKOEIAALEQEIALE 27	
Db	3 LRALKKALKALKALKALKALKALK 28	
	RESULT 35	
	US-08-823-771-36	
	; Sequence 36, Application US/08823771	
	; Patent No. 6459019	
	; GENERAL INFORMATION:	
	; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY	
	; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT	
	; NUMBER OF SEQUENCES: 107	
	; CORRESPONDENCE ADDRESS:	
	; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY	
	; STREET: 1007 MARKET STREET	
	; CITY: WILMINGTON	
	; STATE: DELAWARE	
	; COUNTRY: U.S.A.	
	; ZIP: 19898	
	; COMPUTER READABLE FORM:	
	; MEDIUM TYPE: FLOPPY DISK	
	; COMPUTER: IBM PC COMPATIBLE	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; SOFTWARE: MICROSOFT WORD VERSION 2.0C	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/08/823,771	
	; FILING DATE: 24-Mar-1997	
	; CLASSIFICATION: <Unknown>	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: 08/474,633	
	; FILING DATE: <Unknown>	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: BARBARA C. SIEGELL	
	; REGISTRATION NUMBER: 30,684	
	; REFERENCE/DOCKET NUMBER: BB-1037-C	
	; TELEPHONE: 302-992-4931	
	; TELEFAX: 302-773-0164	
	; TELEX: 835420	
	; INFORMATION FOR SEQ ID NO: 40:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 28 amino acids	
	; TYPE: amino acid	
	; TOPOLOGY: linear	
	; MOLECULE TYPE: protein	
	; SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
	US-08-823-771-40	
	Query Match 26.3%; Score 36; DB 2; Length 28;	
	Best Local Similarity 24.0%; Pred. No. 2.6e+02;	
	Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;	
QY	1 KIRALKKNKAHLKOEIAALEQEIAA 25	
Db	4 KMKAMEEKWKAMEEKWKAMEEKMA 28	
	RESULT 36	
	US-08-823-771-40	
	; Sequence 40, Application US/08823771	
	; Patent No. 6459019	
	; GENERAL INFORMATION:	
	; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY	
	; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT	
	; NUMBER OF SEQUENCES: 107	
	; CORRESPONDENCE ADDRESS:	
	; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY	
	; STREET: 1007 MARKET STREET	
	; CITY: WILMINGTON	
	; STATE: DELAWARE	
	; COUNTRY: U.S.A.	
	; ZIP: 19898	
	; COMPUTER READABLE FORM:	
	; MEDIUM TYPE: FLOPPY DISK	
	; COMPUTER: IBM PC COMPATIBLE	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; SOFTWARE: MICROSOFT WORD VERSION 2.0C	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/08/823,771	
	; FILING DATE: 24-Mar-1997	
	; CLASSIFICATION: <Unknown>	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: 08/474,633	
	; FILING DATE: <Unknown>	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: BARBARA C. SIEGELL	
	; REGISTRATION NUMBER: 30,684	
	; REFERENCE/DOCKET NUMBER: BB-1037-C	
	; TELEPHONE: 302-992-4931	
	; TELEFAX: 302-773-0164	
	; TELEX: 835420	
	; INFORMATION FOR SEQ ID NO: 40:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 28 amino acids	
	; TYPE: amino acid	
	; TOPOLOGY: linear	
	; MOLECULE TYPE: protein	
	; SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
	US-08-823-771-40	
	Query Match 26.3%; Score 36; DB 2; Length 28;	
	Best Local Similarity 24.0%; Pred. No. 2.6e+02;	
	Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;	
QY	1 KIRALKKNKAHLKOEIAALEQEIAA 25	
Db	4 KMKAMEEKWKAMEEKWKAMEEKMA 28	
	RESULT 36	
	US-08-823-771-40	
	; Sequence 40, Application US/08823771	
	; Patent No. 6459019	
	; GENERAL INFORMATION:	
	; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY	
	; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT	
	; NUMBER OF SEQUENCES: 107	
	; CORRESPONDENCE ADDRESS:	
	; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY	
	; STREET: 1007 MARKET STREET	
	; CITY: WILMINGTON	
	; STATE: DELAWARE	
	; COUNTRY: U.S.A.	
	; ZIP: 19898	
	; COMPUTER READABLE FORM:	
	; MEDIUM TYPE: FLOPPY DISK	
	; COMPUTER: IBM PC COMPATIBLE	
	; OPERATING SYSTEM: PC-DOS/MS-DOS	
	; SOFTWARE: MICROSOFT WORD VERSION 2.0C	
	; CURRENT APPLICATION DATA:	
	; APPLICATION NUMBER: US/08/823,771	
	; FILING DATE: 24-Mar-1997	
	; CLASSIFICATION: <Unknown>	
	; PRIOR APPLICATION DATA:	
	; APPLICATION NUMBER: 08/474,633	
	; FILING DATE: <Unknown>	
	; ATTORNEY/AGENT INFORMATION:	
	; NAME: BARBARA C. SIEGELL	
	; REGISTRATION NUMBER: 30,684	
	; REFERENCE/DOCKET NUMBER: BB-1037-C	
	; TELEPHONE: 302-992-4931	
	; TELEFAX: 302-773-0164	
	; TELEX: 835420	
	; INFORMATION FOR SEQ ID NO: 40:	
	; SEQUENCE CHARACTERISTICS:	
	; LENGTH: 28 amino acids	
	; TYPE: amino acid	
	; TOPOLOGY: linear	
	; MOLECULE TYPE: protein	
	; SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
	US-08-823-771-40	


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; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; OTHER INFORMATION: /note= "(SSP 5)4"
PCT-US92-06412-2
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Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 KIRALKWKNHKLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
DB 4 KMKAMEEKMKAMEEKMKAMEEKMK 28
```

```
RESULT 40
PCT-US92-06412-39
; Sequence 39, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-3
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```
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 KIRALKWKNHKLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
DB 4 KMKAMEEKMKAMEEKMKAMEEKMK 28
```

```
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-39
```

```
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
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```
QY 1 KIRALKWKNHKLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
DB 4 KMKAMEEKMKAMEEKMKAMEEKMK 28
```

```
RESULT 41
PCT-US92-06412-43
; Sequence 43, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing P
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-43
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```
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
```

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QY 1 KIRALKWKNHKLKQETAALEQETAA 25
|::|::|::|::|::|::|::|::|
DB 4 KMKAMEEKMKAMEEKMKAMEEKMK 28
```

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PCT-US92-06412-47
; Sequence 47, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing R
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-47

Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWKNAHLKQEIQAALQEIQA 25
; : : : : : : : : : : : : : : : :
Db 4 KKKAMEEKMKAMEEKMKAMEEKMA 28

RESULT 43
US-08-944-133-31
; Sequence 31, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H

PCT-US92-06412-47
; Sequence 47, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; APPLICANT: Janet A. Rice
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing R
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06412
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamethy Floyd
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 992-4929
; TELEFAX: (302) 892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-06412-47

Query Match 25.5%; Score 35; DB 1; Length 28;
Best Local Similarity 34.6%; Pred. No. 3.5e+02;
Matches 9; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 3 RALKWKNAHLKQEIQAALQEIQA 28
; : : : : : : : : : : : : : : : :
Db 1 KALKKALKKALKKALKKALKK 26

RESULT 44
US-08-944-133-35
; Sequence 35, Application US/08944133
; Patent No. 5789542
; GENERAL INFORMATION:
; APPLICANT: McLaughlin, Mark L
; APPLICANT: Becker, Calvin L
; TITLE OF INVENTION: Amphipathic Peptides
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John H. Runnels
; STREET: P. O. Box 2471
; CITY: Baton Rouge
; STATE: LA
; COUNTRY: USA
; ZIP: 70821-2471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,133
; FILING DATE: 06-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/789,077
; FILING DATE: 03-FEB-1997
; APPLICATION NUMBER: US/08/681,075
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Runnels, John H
```

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;
;   REGISTRATION NUMBER: 33451
;   REFERENCE/DOCKET NUMBER: Atty File No. 5789542 9301
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 504 387-3221
;   TELEFAX: 504 346-8049
;   INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 28 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-944-133-35

Query Match      25.5%; Score 35; DB 1; Length 28;
Best Local Similarity 36.0%; Pred. No. 3.5e+02;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
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QY      2 IRALKKNAHLKQEIALLQETAAAL 26
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DB      4 LRALKKALKKALKKALKKALKAL 28
          ::|||
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RESULT 45
US-09-082-279B-377
; Sequence 377, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 377
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-377
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Query Match      25.5%; Score 35; DB 2; Length 28;
Best Local Similarity 43.8%; Pred. No. 3.5e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 KIRALKKNAHLKQEI 16
          |. | | | | | | |
DB      1 KVEELLSKNYHLENEL 16
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Search completed: November 21, 2005, 21:41:32
Job time : 32.5 secs

Result No.	Score	Query Match	Length	PB	ID	Description	
1	81	59.1	28	4	US-10-360-053-23	Sequence 23, Appl	
2	59	43.1	28	4	US-10-360-053-21	Sequence 21, Appl	
3	54	39.4	28	4	US-10-360-053-22	Sequence 22, Appl	
4	45	32.8	28	4	US-10-080-608A-1	Sequence 1, Appl	
5	45	32.8	28	4	US-10-370-685-90	Sequence 90, Appl	
6	45	32.8	28	4	US-10-267-682-84	Sequence 84, Appl	
7	45	32.8	28	4	US-10-267-748-84	Sequence 84, Appl	
8	39	28.5	28	3	US-09-320-907B-6	Sequence 6, Appl	
9	39	28.5	28	4	US-10-447-292-6	Sequence 6, Appl	
10	38	27.7	28	4	US-10-023-066A-70	Sequence 70, Appl	
11	38	27.7	28	5	US-10-804-678-70	Sequence 70, Appl	
12	36	26.3	28	4	US-10-023-066A-36	Sequence 36, Appl	
13	36	26.3	28	4	US-10-023-066A-40	Sequence 40, Appl	
14	36	26.3	28	4	US-10-023-066A-56	Sequence 56, Appl	
15	36	26.3	28	4	US-10-023-066A-67	Sequence 67, Appl	
16	36	26.3	28	5	US-10-804-678-36	Sequence 36, Appl	
17	36	26.3	28	5	US-10-804-678-40	Sequence 40, Appl	
18	36	26.3	28	5	US-10-804-678-56	Sequence 56, Appl	
19	36	26.3	28	5	US-10-804-678-67	Sequence 67, Appl	
20	35	25.5	28	4	US-10-351-641-377	Sequence 377, Appl	
21	34	24.8	28	3	US-09-847-940B-19	Sequence 19, Appl	
22	34	24.8	28	3	US-09-945-917-24	Sequence 24, Appl	
23	34	24.8	28	3	US-09-847-946A-19	Sequence 19, Appl	
24	34	24.8	28	4	US-10-552-244-16	Sequence 16, Appl	
25	34	24.8	28	5	US-10-830-959-6	Sequence 6, Appl	
26	34	24.8	28	5	US-10-979-683-19	Sequence 19, Appl	
27	34	24.8	28	5	US-10-900-399-16	Sequence 16, Appl	

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; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-21

Query Match      43.1%; Score 59; DB 4; Length 28;
Best Local Similarity 40.0%; Pred. No. 0.91;
Matches 10; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

QY 4 ALKWKNAHLKQETIAALEQETIAALEQ 28
Db 1 AIEYEQAIKEETIAINDKIAIKE 25

RESULT 3
US-10-360-053-22
; Sequence 22, Application US/10360053
; Publication No. US20030170230A1
; GENERAL INFORMATION:
; APPLICANT: Caterer, Nigel
; APPLICANT: Uttenhal, Lars O
; APPLICANT: Nielsen, Rasmus W
; TITLE OF INVENTION: Compositions and Methods for Assembly and Stabilization of Antic
; TITLE OF INVENTION: Fragments via Antiparallel Heterogeneous Coiled-Coil Peptide Regi
; TITLE OF INVENTION: Theroef
; FILE REFERENCE: IMX-0028
; CURRENT APPLICATION NUMBER: US/10/360,053
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US60/354,376
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-360-053-22

Query Match      39.4%; Score 54; DB 4; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 12; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KIRALKWKNAHLKQETIAALEQETIA 24
Db 5 KIAAIEKIAQIEETIAAQEEKIA 28

RESULT 4
US-10-080-608A-1
; Sequence 1, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae

US-10-080-608A-1
Query Match      32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 65;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWKNAHLKQETIAALEQ 21
Db 7 KVEELLKKNYHLENEVARLKK 27

RESULT 5
US-10-370-685-90
; Sequence 90, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 28
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: leucine zipper sequence
US-10-370-685-90

Query Match      32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 65;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWKNAHLKQETIAALEQ 21
Db 7 KVEELLKKNYHLENEVARLKK 27

RESULT 6
US-10-267-682-84
; Sequence 84, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
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/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-267-748-84
Query Match 32.8%; Score 45; DB 4; Length 28;
Best Local Similarity 42.9%; Pred. No. 65;
Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKWKNAHLKQEIATAALEQ 21
   | : | | | | | | | | | | : | :
DB 7 KVEELLSKNYHLENEVARLKK 27

RESULT 8
US-09-320-907B-6
; Sequence 6, Application US/09320907B
; Publication No. US20020198360A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PPAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/09/320,907B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-320-907B-6
Query Match 28.5%; Score 39; DB 3; Length 28;
Best Local Similarity 37.0%; Pred. No. 4e+02;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 KIRALKWKNAHLKQEIATAALEQ 27
   | : | | | | | | | | | | : | :
DB 1 KLEALEGRDLALRGKLEALEGKLDAL 27

RESULT 9
US-10-447-292-6
; Sequence 6, Application US/10447292
; Publication No. US20030224453A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PPAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/10/447,292
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/320,907B
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

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; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-10-447-292-6

Query Match      28.5%; Score 39; DB 4; Length 28;
Best Local Similarity 37.0%; Pred. No. 4e+02;
Matches 10; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQETIAALEQETIAA 27
Db 1 KLEALEGRDLAEGKLEALEGKLDAL 27

RESULT 10
US-10-023-066A-70
; Sequence 70, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-023-066A-70

Query Match      27.7%; Score 38; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQETIAALEQETIAA 25
Db 1 KLEALEGRDLAEGKLEALEGKLDAL 27

RESULT 11
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US200500530A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match      27.7%; Score 38; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQETIAALEQETIAA 25
Db 4 KLEALEGRDLAEGKLEALEGKLDAL 28

RESULT 12
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
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Db 4 KLEALEGRDLAEGKLEALEGKLDAL 28

RESULT 11
US-10-804-678-70
; Sequence 70, Application US/10804678
; Publication No. US200500530A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION: /label= name
; /note= "(SSP 7)4"
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-804-678-70

Query Match      27.7%; Score 38; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWKNHLKQETIAALEQETIAA 25
Db 4 KLEALEGRDLAEGKLEALEGKLDAL 28

RESULT 12
US-10-023-066A-36
; Sequence 36, Application US/10023066A
; Publication No. US20030056242A1
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;
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
;
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIHALEQEIHA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28

;
; RESULT 13
; US-10-023-066A-40
; Sequence 40, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
;
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-023-066A-36
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIHALEQEIHA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28

;
; RESULT 14
; US-10-023-066A-56
; Sequence 56, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
;
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
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;
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-023-066A-40
Query Match 26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIHALEQEIHA 25
Db 4 KMKAMEEKMKAMEEKMKAMEEKMA 28

;
; RESULT 14
; US-10-023-066A-56
; Sequence 56, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
;
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
;
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-023-066A-56

Query Match      26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEIATALEQEIAA 25
|:::| |:::| |:::|
4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28

DB

RESULT 15
US-10-023-066A-67
; Sequence 67, Application US/10023066A
; Publication No. US20030056242A1
; GENERAL INFORMATION:
; APPLICANT: E. I. DU PONT DE NEMOURS AND COMPANY
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE AND THREONINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD VERSION 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,066A
; FILING DATE: 29-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BARBARA C. SIEGELL
; REGISTRATION NUMBER: 30,684
; REFERENCE/DOCKET NUMBER: BB-1037-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4931
; TELEFAX: 302-773-0164
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..28
; OTHER INFORMATION:
; /note= "(ISSP 5)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-023-066A-67

Query Match      26.3%; Score 36; DB 4; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEIATALEQEIAA 25
|:::| |:::| |:::|
4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28

DB

RESULT 16
US-10-804-678-36
; Sequence 36, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-804-678-36

Query Match      26.3%; Score 36; DB 5; Length 28
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0;

QY 1 KIRALKWNAHLKQEIATALEQEIAA 25
|:::| |:::| |:::|
4 KMKAMEEKWKAMEEKWKAMEEKWKMA 28

DB

RESULT 17
US-10-804-678-40
; Sequence 40, Application US/10804678
; Publication No. US20050005330A1
; GENERAL INFORMATION:
; APPLICANT: EPELBAUM, SABINE URSULA
; FALCO, SAVERIO CARL
; MCDEVITT, RAYMOND ERVIN, III
; TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT OFFICE 97
; SOFTWARE: MICROSOFT WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/804,678
; FILING DATE: 19-Mar-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,304
; FILING DATE: 27-Mar-1998
; APPLICATION NUMBER: 08/824,627
; FILING DATE: MARCH 27, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1037-F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-892-7949
; TELEX: 835420
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-804-678-36

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/
/
/ TELEFAX: 302-892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 67:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ FEATURE:
/
/ NAME/KEY: Protein
/ LOCATION: 1..28
/ OTHER INFORMATION: /label= name
/ /note= "(SSP 5)4"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-804-678-67

Query Match 26.3%; Score 36; DB 5; Length 28;
Best Local Similarity 24.0%; Pred. No. 1e+03;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEIATAALPQEIATA 25
Db 4 KWKAMEEKWKAMEEKWKAMEEKWKMA 28

RESULT 20
US-10-351-641-377
/ Sequence 377, Application US/10351641
/ Publication No. US20030186874A1
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ TITLE OF INVENTION: PROPERTIES
/ FILE REFERENCE: 7872-100
/ CURRENT APPLICATION NUMBER: US/10/351,641
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/350,641
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: 09/315,304
/ PRIOR FILING DATE: 1998-05-20
/ PRIOR APPLICATION NUMBER: 09/082,279
/ NUMBER OF SEQ ID NOS: 1757
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 377
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-10-351-641-377

Query Match 25.5%; Score 35; DB 4; Length 28;
Best Local Similarity 43.8%; Pred. No. 1.4e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KIRALKWNAHLKQEI 16
Db 1 KVEELLKKNYHLENEL 16

RESULT 21
US-09-847-940B-19
/ Sequence 19, Application US/09847940B
/ Patent No. US20020156000A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J.
/ APPLICANT: Ghosh, Sankar
/ APPLICANT:

Query Match 24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 3 RALKWNAHLKQEIATALEQ 22
Db 11 RRMWKKTAL--DASALQTE 28

RESULT 22
US-09-945-917-24
/ Sequence 24, Application US/09945917
/ Publication No. US20030042381A1
/ GENERAL INFORMATION:
/ APPLICANT: Bogaert, Thierry
/ APPLICANT: Vandekerckhove, Joel
/ TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
/ TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
/ TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
/ FILE REFERENCE: P/14-1
/ CURRENT APPLICATION NUMBER: US/09/945,917
/ CURRENT FILING DATE: 1998-09-21
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-09-945-917-24

Query Match 24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 38.9%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 IRALKWNAHLKQEIATAAL 19
Db 5 VNKLKTKENKQLKKEVDKL 22

RESULT 23
US-09-847-946A-19
/ Sequence 19, Application US/09847946A
/ Publication No. US20030054999A1
/ GENERAL INFORMATION:
/ APPLICANT: May, Michael J
/ APPLICANT: Ghosh, Sankar
/ APPLICANT: Findeis, Mark A
/ APPLICANT: Phillips, Kathryn
/ APPLICANT: Hannig, Gerhard
/ TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
/ FILE REFERENCE: PPI-119
/ CURRENT APPLICATION NUMBER: US/09/847,946A
/ CURRENT FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,261
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 09/643,260
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; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-19

Query Match      24.8%; Score 34; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Qy      3 RALKWKNHLKQEIATALEQE 22
Db      11 RRMWKKTKAL--DASALQTE 28

RESULT 24
US-10-652-244-16
; Sequence 16, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-652-244-16

Query Match      24.8%; Score 34; DB 4; Length 28;
Best Local Similarity 39.1%; Pred. No. 1.9e+03;
Matches 9; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

Qy      10 AHLKQEIATALEQEI----AALEQ 28
Db      3 ASLRQQLALQGLQHLQALSQ 25

RESULT 25
US-10-830-959-6
; Sequence 6, Application US/10830959
; Publication No. US20040259201A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Howard
; APPLICANT: Nadesalingam, Palaniyar
; APPLICANT: Reid, Kenneth
; APPLICANT: Strong, Peter
; TITLE OF INVENTION: Recombinant Surfactant Protein D Compositions and Methods of Use
; FILE REFERENCE: 18396/2402
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; CURRENT APPLICATION NUMBER: US/10/830,959
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: PCT/GB02/04824
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: GB 0125638.7
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: GB 0209619.6
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-830-959-6

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 6; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy      10 AHLKQEIATALEQEIATALE 27
Db      3 ASLRQQLALQGLQVQHLQ 20

RESULT 26
US-10-979-683-19
; Sequence 19, Application US/10979683
; Publication No. US20050143302A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-117CPDV
; CURRENT APPLICATION NUMBER: US/10/979,683
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: 09/847,940
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptides
US-10-979-683-19

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

Qy      3 RALKWKNHLKQEIATALEQE 22
Db      11 RRMWKKTKAL--DASALQTE 28

RESULT 27
US-10-900-399-16
; Sequence 16, Application US/10900399
; Publication No. US20050158823A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
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```
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-16

Query Match      24.8%; Score 34; DB 5; Length 28;
Best Local Similarity 39.1%; Pred. No. 1.9e+03;
Matches 9; Conservative 6; Mismatches 4; Indels 4; Gaps 1;

QY      10 AHLKQEIQALEQEI-----AALEQ 28
      ||::||::||::||::||
Db       3 ASLRQQLAALQGLQHLQAALSQ 25

RESULT 28
US-11-032-630-32
; Sequence 32, Application US/11032630
; Publication No. US20050208036A1
; GENERAL INFORMATION:
; APPLICANT: Blazer, Bruce R
; APPLICANT: O'Shaughnessy, Mathew J
; APPLICANT: Vogtenhuber, Christine
; APPLICANT: Serody, Jonathan S
; APPLICANT: Albert, Baldwin S
; TITLE OF INVENTION: METHODS FOR TREATING OR PREVENTING GVHD
; FILE REFERENCE: 421/115/2
; CURRENT APPLICATION NUMBER: US/11/032,630
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 10/374,222
; PRIOR FILING DATE: 2003-02-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant non-functional MTD-NBD fusion polypeptide
US-11-032-630-32

Query Match      24.8%; Score 34; DB 6; Length 28;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 8; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY      3 RALKWKNAHLKQEIQALEQ 22
      ||::||::||::||::||
Db      11 RRWKWKKTAL--DASALQTE 28

RESULT 29
US-09-864-761-42292
; Sequence 42292, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42292
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008392.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
US-09-864-761-42292

Query Match      24.5%; Score 33.5; DB 3; Length 28;
Best Local Similarity 34.6%; Pred. No. 2.2e+03;
Matches 9; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY      3 RALKWKNAHLKQEIQALEQ 28
      ||::||::||::||::||
Db       3 RLLKGR-AQVQAEIEELQETRALDK 27

RESULT 30
US-10-267-682-85
; Sequence 85, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
```

```
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-682-85
Query Match 24.1%; Score 33; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 2.5e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Qy 5 LKWNHKLKQRIALAEQRIAL 26
Db 4 LQAEQDEKSAEQRIAL 25
RESULT 31
US-10-267-748-85
Sequence 85, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-267-748-85
Query Match 24.1%; Score 33; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 2.5e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
Qy 5 LKWNHKLKQRIALAEQRIAL 26
Db 4 LQAEQDEKSAEQRIAL 25
RESULT 32
US-10-023-066A-58
Sequence 58, Application US/10023066A
Publication No. US20030056242A1
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
COMPANY
TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
INCREASING THE LYSINE AND
THREONINE CONTENT OF THE SEEDS OF
PLANTS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,066A
FILING DATE: 29-Apr-2002
```

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/
/
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BARBARA C. SIEGELL
/ REGISTRATION NUMBER: 30,684
/ REFERENCE/DOCKET NUMBER: BB-1037-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-4931
/ TELEFAX: 302-773-0164
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-023-066A-58

Query Match      23.4%; Score 32; DB 4; Length 28;
Best Local Similarity 20.0%; Pred. No. 3.4e+03;
Matches 5; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETIAALEQETAA 25
   |::||:|::||:|::||:|
Db 4 KMKAMEEKLKMKEEKLKMKEEKMKA 28

RESULT 33
US-10-652-244-17
/ Sequence 17, Application US/10652244
/ Publication No. US20040052788A1
/ GENERAL INFORMATION:
/ APPLICANT: Wiley, Steven R.
/ TITLE OF INVENTION: Cytokine that Induces Apoptosis
/ FILE REFERENCE: 2835-E
/ CURRENT APPLICATION NUMBER: US/10/652,244
/ PRIOR FILING DATE: 2003-09-02
/ PRIOR APPLICATION NUMBER: US/09/796,581
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: 09/320,424
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 09/190,046
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 09/048,641
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 08/670,354
/ PRIOR FILING DATE: 1996-06-25
/ PRIOR APPLICATION NUMBER: 08/548,368
/ PRIOR FILING DATE: 1995-11-01
/ PRIOR APPLICATION NUMBER: 08/496,632
/ PRIOR FILING DATE: 1995-06-29
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: LZ peptide
US-10-652-244-17

Query Match      23.4%; Score 32; DB 4; Length 28;
Best Local Similarity 34.8%; Pred. No. 3.4e+03;
Matches 8; Conservative 7; Mismatches 4; Indels 1;

QY 10 AHLKQETIAALEQETIAALEQETAA 28
   |::||:|::||:|::||:|
Db 3 ASIRQQETIALEQETIAALEQETAA 25

RESULT 34
US-10-804-678-58
/ Sequence 58, Application US/10804678
/ Publication No. US20050005330A1
```

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/
/
/ GENERAL INFORMATION:
/ APPLICANT: EPELBAUM, SABINE URSULA
/ FALCO, SAVERIO CARL
/ MCDONNELL, RAYMOND ERVIN, III
/ TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
/ INCREASING THE LYSINE CONTENT OF
/ THE SEEDS OF PLANTS
/
/ NUMBER OF SEQUENCES: 132
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
/ STREET: 1007 MARKET STREET
/ CITY: WILMINGTON
/ STATE: DELAWARE
/ COUNTRY: U.S.A.
/ ZIP: 19898
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.50 INCH
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MICROSOFT OFFICE 97
/ SOFTWARE: MICROSOFT WINDOWS 95
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/804,678
/ FILING DATE: 19-Mar-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/049,304
/ FILING DATE: 27-Mar-1998
/ APPLICATION NUMBER: 08/824,627
/ FILING DATE: MARCH 27, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CHRISTENBURY, LYNNE M.
/ REGISTRATION NUMBER: 30,971
/ REFERENCE/DOCKET NUMBER: BB-1037-F
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 302-992-5481
/ TELEFAX: 302-892-7949
/ TELEX: 835420
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-804-678-58

Query Match      23.4%; Score 32; DB 5; Length 28;
Best Local Similarity 20.0%; Pred. No. 3.4e+03;
Matches 5; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 KIRALKKNAHLKQETIAALEQETIAA 25
   |::||:|::||:|::||:|
Db 4 KMKAMEEKLKMKEEKLKMKEEKMKA 28

RESULT 35
US-10-900-399-17
/ Sequence 17, Application US/10900399
/ Publication No. US20050158823A1
/ GENERAL INFORMATION:
/ APPLICANT: Wiley, Steven R.
/ APPLICANT: Goodwin, Raymond G.
/ TITLE OF INVENTION: Cytokine that Induces Apoptosis
/ FILE REFERENCE: 2835-E
/ CURRENT APPLICATION NUMBER: US/10/900,399
/ CURRENT FILING DATE: 2004-07-28
/ PRIOR APPLICATION NUMBER: US/09/796,581
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: 09/320,424
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: 09/190,046
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: 09/048,641
```


; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: LZ peptide
US-10-900-399-17

Query Match 23.4%; Score 32; DB 5; Length 28;
Best Local Similarity 34.8%; Pred. No. 3.4e+03;
Matches 8; Conservative 7; Mismatches 4; Indels 4; Gaps 1;

Qy 10 AHLKQETIAALEQEI-----ALEQ 28
Db 3 ASIRQQIEAIGQIQHTQAISQ 25

RESULT 36
US-09-864-761-43156
; Sequence 43156, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43156
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049565.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.81
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 0.94
; OTHER INFORMATION: EST_HUMAN HIT: AW821909.1, EVALUOE 2.70e-02
US-09-864-761-43156

Query Match 22.6%; Score 31; DB 3; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEI 16
Db 14 LQWNGFLKIEL 25

RESULT 37
US-10-252-136-16
; Sequence 16, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-16

Query Match 22.6%; Score 31; DB 4; Length 28;
Best Local Similarity 29.4%; Pred. No. 4.6e+03;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 WKNAHLKQETIAALEQEI 23
Db 8 WKDLKSLLEVKDEL 24

RESULT 38
US-10-351-641-494
; Sequence 494, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

Query Match	22.6%;	Score 31;	DB 4;	Length 28;
Best Local Similarity	29.4%;	Pred. No. 4.6e+03;		

Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 7 WKNAHLKQEIATLAEQEI 23

Db 8 WKDLKSLLEVDKDEL 24

RESULT 41

US-09-746-742-25
; Sequence 25, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Soluble, Trimeric Version of the Coiled Coil
; OTHER INFORMATION: Region to GCN4 in IQN17
US-09-746-742-25

Query Match 21.9%; Score 30; DB 3; Length 28;
Best Local Similarity 28.6%; Pred. No. 6.3e+03;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KIRALKWNAHLKQEIATLAEQ 21

Db 8 KIEETESKQKKIENIARIKK 28

RESULT 42

US-10-080-608A-2
; Sequence 2, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Unknown

; FEATURE:
; OTHER INFORMATION: Probable variant of hómo sapiens protein.
US-10-080-608A-2

Query Match 21.9%; Score 30; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 6.3e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEIATLAEQEIATL 26

Db 4 LQAEITDQLEDEKVALQTEIATL 25

RESULT 43

US-10-370-685-91
; Sequence 91, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF-P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 28
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: leucine zipper sequence
US-10-370-685-91

Query Match 21.9%; Score 30; DB 4; Length 28;
Best Local Similarity 40.9%; Pred. No. 6.3e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 5 LKWKNAHLKQEIATLAEQEIATL 26

Db 4 LQAEITDQLEDEKVALQTEIATL 25

RESULT 44

US-10-267-682-86
; Sequence 86, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
; COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

Tue Nov 22 08:14:37 2005

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; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-831

Query Match      13.1%; Score 18; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      8 KNAHLK 13
Db      16 KTAVMK 21

RESULT 5
US-10-632-349-4
; Sequence 4, Application US/10632349
; Publication No. US20050250685A1
; GENERAL INFORMATION:
; APPLICANT: ZAVERI, CHANDA
; TITLE OF INVENTION: PEPTIDES WITH WOUND HEALING ACTIVITY
; FILE REFERENCE: 37896.00002.DIV3
; CURRENT APPLICATION NUMBER: US/10/632.349
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: 09/879,666
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/211,859
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: Acetylation
US-10-632-349-4

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      12 LKEBIALEQ 21
Db      16 LKEKKEVVEE 25

RESULT 6
US-10-939-890-345
; Sequence 345, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KOR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351

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; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 345
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-345

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      7 WKNAHLK 13
Db      7 WTPHPK 13

RESULT 7
US-10-939-890-351
; Sequence 351, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 351

```

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; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-351

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 23.1%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY      7 WKNAHLKQETAAAL 19
Db      10 WEQVVLHDDAQVL 22

RESULT 8
US-10-939-890-382
; Sequence 382, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin UU spacer linker
US-10-939-890-698

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KW 7
Db      10 KW 11

RESULT 10
US-10-939-890-821
; Sequence 821, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
```

```
RESULT 9
US-10-939-890-698
; Sequence 698, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 698
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin UU spacer linker
US-10-939-890-698

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KW 7
Db      10 KW 11
```

```
Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KW 7
Db      10 KW 11
```

```
RESULT 10
US-10-939-890-821
; Sequence 821, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
```



```

; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 821
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (13)..(13)
; OTHER INFORMATION: Lys residue modified with a iv-dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-821

```

```

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 42.9%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 7 WKNAHLK 13
Db 7 WTPHPK 13

```

```

RESULT 11
; Sequence 827, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong

```

```

; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 827
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-827

```

```

Query Match      11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 23.1%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy 7 WKNAHLKQETAAAL 19
Db 10 WEQVVLHDDAQVL 22

```

```

RESULT 12
US-10-997-201A-13
; Sequence 13, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-13

```

Query Match 11.7%; Score 16; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 5; Indels

Qy	10	AHLKQEIAALEQ	21
		: : :	
Dp	6	AYKODEKVASDO	17

RESULT 13

US-10-939-890-353
; Sequence 353, Application US/10939890
; Publication No. US20050250700A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US 10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 384
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
/ US-10-939-890-384

```

Query Match 10.9%; Score 15; db 1; Length 28;
Best Local Similarity 30.0%; Pred. No. 2e+03;
Matches 3: Conservative 2: Mismatches 5: Indels

Qy 6 KWKNAHLKQE 15
: | : |
Db 2 OWYHDGLHNE 11

RESULT 15

US-10-939-890-829
; Sequence 829, Application US/10939890
; Publication No. US20050250700A1

FEATURE: ;
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-353

Query Match 10.9%; Score 15; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 2: Conservative 0; Mismatches 1; Indels

Qy 7 WKN 9
|
p'b 11 WLN 13

RESULT 14

US-10-939-890-384
; Sequence 384, Application US/10939890
; Publication No. US20050250700A1

GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.

```

; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
; US-10-939-890-829

Query Match          10.9%; Score 15; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      7 WKN 9
      |||
Db     11 WLN 13

RESULT 16
; Sequence 213, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 213
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (DNA binding domain)
; US-11-096-706-213

Query Match          10.9%; Score 15; DB 7; Length 28;
Best Local Similarity 33.3%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      8 KNAHLKQEI 16
```

```

Db     12 RSDHLTTHI 20
      |||

RESULT 17
; US-10-939-890-325
; Sequence 325, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
; US-10-939-890-325

Query Match          10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      7 WKN 9
      |||
Db     12 WRS 14

RESULT 18
; US-10-939-890-326
; Sequence 326, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
```

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 326
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-326

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QEI 16
Db 10 QEI 12

RESULT 19
US-10-939-890-344
/ Sequence 344, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 326
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-326
```

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 344
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ALKW 7
Db 7 AQQM 10

RESULT 20
US-10-939-890-356
/ Sequence 356, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 356
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-344
```

```
; FEATURE:
; OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-356

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
Db      8 EILSMADQL 16

RESULT 21
US-10-939-890-630
; Sequence 630, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a JJ spacer linker
US-10-939-890-630

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
Db      8 EILSMADQL 16

US-10-939-890-719
; Sequence 719, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 719
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-719

Query Match      10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 4.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      15 EIAALEQEI 23
Db      8 EILSMADQL 16

RESULT 23
US-10-939-890-721
; Sequence 721, Application US/10939890
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; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 721
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
US-10-939-890-721
```

```
Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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```
QY 15 EIAALEQEI 23
DB 8 EILSMADQL 16
```

```
RESULT 24
US-10-939-890-722
; Sequence 722, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
```

```
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 722
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-722
```

```
Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 15 EIAALEQEI 23
DB 8 EILSMADQL 16
```

```
RESULT 25
US-10-939-890-794
; Sequence 794, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
```

; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with SATA linker
US-10-939-890-794

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 15 EIAALEQEI 23
|| : : :
Db 8 EILSMADQL 16

RESULT 26
US-10-939-890-795
; Sequence 795, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 795
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with SATA JJ spacer linker
US-10-939-890-795

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 15 EIAALEQEI 23
|| : : :
Db 8 EILSMADQL 16

RESULT 27
US-10-939-890-820
; Sequence 820, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; CURRENT APPLICATION NUMBER: US 60/440,411

```
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 820
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(4)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-820

Query Match          10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ALKW 7
Db | : |
7 AQQW 10

RESULT 28
US-10-939-890-832
; Sequence 832, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 832
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (3)..(4)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-832
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 832
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-832

Query Match          10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 15 EIAALEQEII 23
Db || : :
8 EILSMADQL 16

RESULT 29
US-10-939-890-847
; Sequence 847, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nannjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 847
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
```


NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a J spacer linker
US-10-939-890-847

Query Match 10.2%; Score 14; DB 1; Length 28;
Best Local Similarity 22.2%; Pred. No. 2.6e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 15 EIAALEQEI 23
|| : :
Db 8 EILSMADQL 16

RESULT 30
US-11-021-441-50
Sequence 50, Application US/11021441
Publication No. US20050249748A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY, Thomas W., Jr.
APPLICANT: PORTNOY, Daniel A., Jr.
APPLICANT: LUCKETT, William S., Jr.
APPLICANT: COOK, David N.
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 282172003900
CURRENT APPLICATION NUMBER: US/11/021.441
CURRENT FILING DATE: 2004-12-23
PRIOR FILING DATE: 2004-10-06
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/615,287
PRIOR FILING DATE: 2004-10-01
PRIOR APPLICATION NUMBER: US 60/599,377
PRIOR FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: PCT/US2004/23881
PRIOR FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US 10/883,599
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 60/556,744
PRIOR FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 28
TYPE: PRT
ORGANISM: Bacillus anthracis
US-11-021-441-50

Query Match 10.2%; Score 14; DB 7; Length 28;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 12 LKQEI AAL 19
|| : :
Db 4 LKQASCAL 11

RESULT 31
US-10-939-890-346
Sequence 346, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 346
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-346

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 ALE 20
|| : :
Db 4 ALE 6

RESULT 32
US-10-939-890-383
Sequence 383, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 383
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-383

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db ||||
4 ALE 6

RESULT 33

US-10-939-890-699
; Sequence 699, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 28
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (28)-(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
; US-10-939-890-699

Query Match 9.5%; Score 13; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db ||||
4 ALE 6

RESULT 34

US-10-939-890-822
; Sequence 822, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 822
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:

```
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: Lys residue modified with a iv-Dde linker
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (26)..(28)
; OTHER INFORMATION: Lys residue modified with Biotin JV spacer linker
US-10-939-890-822

Query Match
Best Local Similarity 9.5%; Score 13; DB 1; Length 28;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 ALE 20
Db 4 ALE 6

RESULT 35
US-11-109-161-3
; Sequence 3, Application US/11109161
; Publication No. US20050244422A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; APPLICANT: SINGH, Baljit K.
; TITLE OF INVENTION: METHODS FOR DELIVERING MED
; TITLE OF INVENTION: PEPTIDE-LINKED AGENT INTO CELLS UNDER CONDITIONS OF CELLULAR
; TITLE OF INVENTION: STRESS
; FILE REFERENCE: 51490-20003.00
; CURRENT APPLICATION NUMBER: US/11/109,161
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/563,141
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/563,676
; PRIOR FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/657,826
; PRIOR FILING DATE: 2005-03-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-109-161-3

Query Match
Best Local Similarity 9.5%; Score 13; DB 7; Length 28;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RALKW 7
Db 18 RGFCW 22

RESULT 36
US-10-986-501-294
; Sequence 294, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
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; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 294
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-294

Query Match
Best Local Similarity 8.8%; Score 12; DB 1; Length 28;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 HL 12
Db 15 HL 16

RESULT 37
US-10-939-890-385
; Sequence 385, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 385
; LENGTH: 28
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-385

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ALKW 7
| |
Db 1 AQDW 4

RESULT 38

US-10-939-890-464
; Sequence 464, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.

; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617, 70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 464

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Library Isolate

US-10-939-890-464

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 KW 7
: |
Db 2 EW 3

RESULT 39

US-10-939-890-701
; Sequence 701, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.

; APPLICANT: Von Wronski, Mathew A.

; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

; FILE REFERENCE: D0617, 70014US00

; CURRENT APPLICATION NUMBER: US/10/939,890

; CURRENT FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: US 10/661,156

; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: PCT/US03/06731

; PRIOR FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/440,411

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/360,851

; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 883

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 701

; LENGTH: 28

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; NAME/KEY: MOD RES

; LOCATION: (1)..(1)

; OTHER INFORMATION: ACETYLATION

; NAME/KEY: MOD RES

; LOCATION: (28)..(28)

; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker

US-10-939-890-701
Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ALKW 7
| |
Db 1 AQDW 4

RESULT 40

US-10-939-890-720
; Sequence 720, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 720
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-720

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KW 7
Db 2 EW 3

RESULT 41
US-10-939-890-723
Sequence 723, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 723
LENGTH: 28
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
FEATURE:
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLTATION
FEATURE:
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Lys residue modified with a SATA linker
US-10-939-890-723

Query Match 8.8%; Score 12; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.2e+03;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KW 7
Db 2 EW 3

RESULT 42
US-11-022-562-236
Sequence 236, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 236
LENGTH: 28
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-236

Query Match 8.8%; Score 12; DB 7; Length 28;

Best Local Similarity 50.0%; Pred. No. 4.2e+03; Indels 0; Gaps 0;
Matches 2; Conservative 2; Mismatches 0;

QY 17 AALE 20
|:::
Db 24 AAMQ 27

RESULT 43

US-10-716-189-10
; Sequence 10, Application US/10716189
; Publication No. US20050249750A1
; GENERAL INFORMATION:
; APPLICANT: Nardin, Elizabeth
; APPLICANT: Moreno, Alberto
; TITLE OF INVENTION: UNIVERSAL T-CELL EPITOPES FOR ANTI-MALARIAL VACCINES
; FILE REFERENCE: 5986/1B615-US1
; CURRENT APPLICATION NUMBER: US/10/716,189
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/060,450
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: 60/033,916
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion of Carboxyl Terminus of SEQ ID NO:4 to
; OTHER INFORMATION: Amino Terminus of Seq ID NO: 1, designated T1B
US-10-716-189-10

Query Match 8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 NAH 11
|:::
Db 1 NAN 3

RESULT 44

US-10-939-890-474
; Sequence 474, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11

; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-474

Query Match 8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 W 7
| W 1
Db 1 W 1

RESULT 45

US-10-939-890-726
; Sequence 726, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide

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; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Lys residue modified with a Biotin JJ spacer linker
US-10-939-890-726

Query Match      8.0%; Score 11; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 W 7
      |
Db      1 W 1

Search completed: November 21, 2005, 22:04:16
Job time : 4.5 secs

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